

STIC Search Report Biotech-Chem Library

STIC Database Tracking Comme

TO: Minh-Tam Davis

Location: rem/3A24/3C18

Art Unit: 1642

Wednesday, April 26, 2006

Case Serial Number: 09/762577

From: Toby Port

Location: Biotech-Chem Library

REM-1A59

Phone: (571)272-2523

toby.port@uspto.gov

Searen Nores

Dear Examiner Davis,

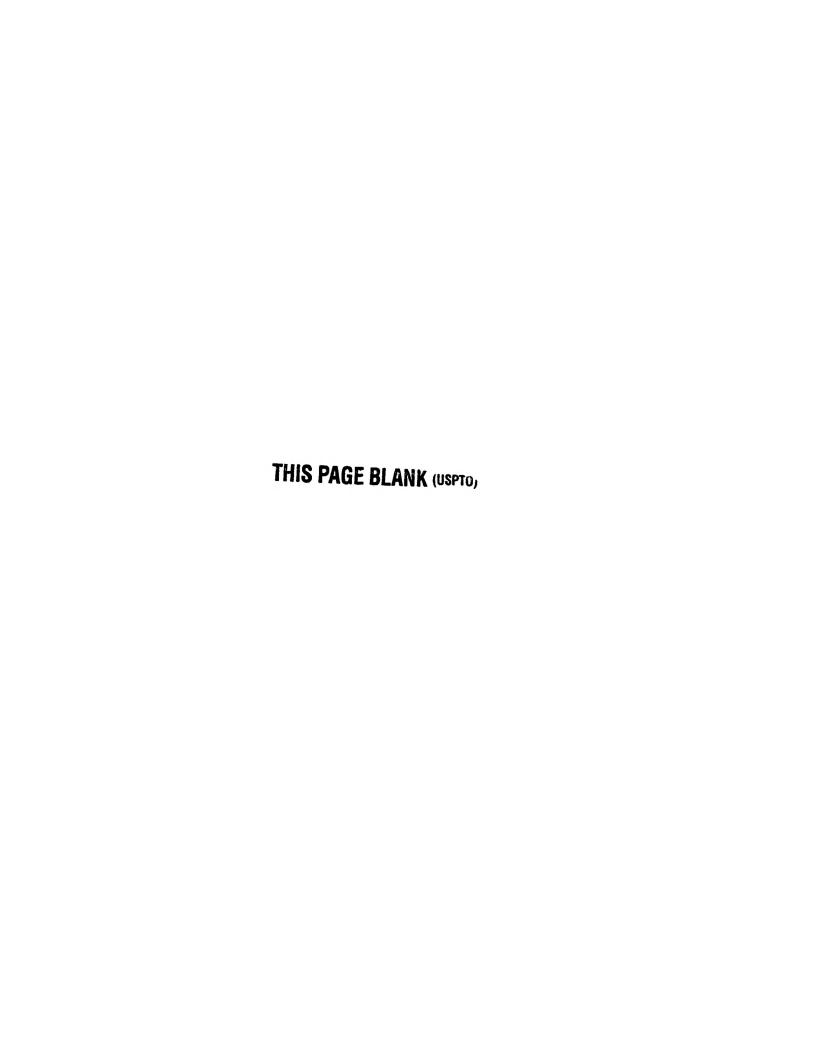
See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port Technical Information Specialist STIC Biotech/Chem Library (571)272-2523





iotech/ChemLib

Chan, Christina

Sent:

Thursday, April 20, 2006 6:34 PM

To: Subject: Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/762577

Please costs. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

----Original Message-----

From:

Davis, Minh-Tam

Sent:

Thursday, April 20, 2006 10:40 AM

To:

Chan, Christina

Subject:

Rush search request for 09/762577

Please search in commercial database, issued patent files, pGPUB and interference:

1) Oligomer search for SEQ ID NO:11

2) Oligomer search for the nucleic acid encoding SEQ ID NO:12.

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 3A24, MB 3C18

272-0830

Searcher:	
Searcher Phone:	
Date Searcher Picked up:_	
Date completed:	
Searcher Prep Time:	
Online Time:	_

Type of Search									
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Encode/Transl:									
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endors and cost where applicable
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Kasof,G.M. and Gomes,B.C.
Livin, a novel inhibitor of apoptosis protein
J. Biol. Chem. 276 (5), 3238-3246 (2001)
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/gene="LIVIN"
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/translation="MGPKDSAKCLHRGPQPSHWAAGDGPTQERCGPRSLGSPVLGLDTCRAWHYDGQLLGQLRPLTEEEEEEGAGATLSRGPAFPGMGSEELRLASFYDWPLTAEVPELLHASGFFCYGGLQSWKKGDDDWTEHAAGFFLLRSKGRDFVPELLRSKGRDFVHSVQETHSQLLGSWDFWEEPEDAAPVAPSVPASGYPELPTPRREVQSESAQEPGARDVEAQLRRLGEERTCKVCLDRAVSIVFVPCGHLVCAECAPGLQLCPICRAPVRSRVRTFLS"
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SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Eraniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

E 1 (bases 1 to 1301)

S Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,

Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,

Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,

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Effort to Identify Novel Human Secreted and Transmembrane Proteins:

AL Genome Res. 13 (10), 2265-2270 (2003)
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AY358835
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Butz.K., Crnkovic-Mertens,I. and Hoppe-Seyler,F.
LIVIN-SPECIFIC siRNAS FOR THE TREATMENT OF THERAPY-RESISTANT
Patent: WO 2004091388-A 10 28-CCT-2004,
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ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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TITLE
JOURNAL
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AUTHORS
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakeeley, R.W., Touchman, J.W., Green, B.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA semences
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                                                                                                                    Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC014475
                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                      Strausberg, R
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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/notte="synonyms: ML-IAP, K
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149-..1045
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/product="Livin inhibitor o
/protein_id="AAH14475_1"
/db_xref="GI:15680241"
/db_xref="GeneID.79444"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'mol_type="mRNA"
'db_xref="taxon:9606"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
..BC.Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy L Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Mor Teika Olson, Diana Palmquiet, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra. Liao,

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: f Column: This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536419. Location/Qualifiers /db_xref="MIM:605737"
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DFVHSYQETHSQLLGSWDPWESPEDAAPVAFSYPASGYFELFTPRREVQSESAQEFGG
VSPAQAQRAWWYLEPGRAFDVEAQLRRLQEERTCKVCLDRAVSIVFVPCGHLVCAECA
PGLQLCPICRAPVRSRVRTFLS" /clone="MGC:23131 IMAGE:4859588" /tlssue type="Skin, melanotic melanoma, /clone lib="NNH MGC 49" /lab_host="DH10B-R" KIAP, LIVIN, RNF50, MLIAP" of apoptosis, isoform

TCTCTGGGCAGCCCTGTCCTAGGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGG 318 CCACAGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGC GTCAGAGCCAGTGTTCCCTCCATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGA GTCAGAGCCAGTGTTCCCTCCATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGA AAGGGCCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACCTG 138 GGCAGGCCTGTGCCTATCCCTGCTGTCCCCAGGGTGGGCCCCGGGGGTCAGGAGCTCCAG CCACAGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGC AAGGGCCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCATTTCTGCTGCAAACCTG 0; Indels 0; Gaps 198 187 247 258 127 67 0

Length 1312;

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22 1 (bases 1 to 1370)

23 Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale and Bioinformatics Assessment.
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/protein_id="AAQ89195.1"
/db_xref="GI:37182790"
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/note="PRO21344"
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/clone="DNA172970"
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100.0%; Pred. No. 0;
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Matches 833; Conserv
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

E 1 (bases 1 to 840)

IE 1 (bases 1 to 840)

S Tanaka, H. and Kaieda, I.

Survivin-like polypeptide and its DNA
Survivin-like polypeptide and its DNA

L Patent: WO 0233071-A 5 25-APR-2002;

TAKEDA CHEMICAL INDUSTRIES LTD, HIROSHI TANAKA, ISAO KAIEDA

OS Homo sapiens (human)

PO 0233071-A/5

PD 25-APR-2002

PF 16-OCT-2001 WO 2001JP009071

PF 16-OCT-2000 JP 00P 316721, 20-DEC-2000 JP 00P 386809 PI
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PC A61K38/17,A61K39/395,A61K48/00,A61P35/00,A61P43/00
Survivin-like polypeptide and its DNA
FH Key
FT source 1.840
FT forganism='Homo sapiens (human)'.
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BD167853
BD167853.1 GI:27873665
WO 0233071-A/5.
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PC
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  GTGCCACCCGAGCTGCTGCTGCCGGCTTCTTCCACACAGGCCATCAGGACAAGGTG
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16-OCT-2001 WO 2001JP009071
17-OCT-2000 JP 00P 316721,20-DEC-2000 JP 00P
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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PO JP 21
PD 10-DD
PF 16-OO
PF HIGO
PC C12NI
PC A61PC
PC A61PC
C12NI
PC C12NI
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Tanaka, H. and Kaieda, I.
Tanaka, H. and Kaieda, I.
Survivin-like polypeptide and its DNA
Patent: JP 2002355062-A 5 10-DEC-2002;
TAKEDA CHEMICAL INDUSTRIES LTD
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Homo sapiens
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JP 2002355062-A/5.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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p 2002355062-A/5
10-DEC-2002
16-OCT-2001 JP 2001318533
HIROSHI TANAKA, ISAO KAIEDA
C12N15/09, A61K31/7088, A61K38/55, A61K39/395, A61K39/395, A61K48/
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A61P43/00,A61P43/00,C07K14/82,C07K16/32,C12N1/15,C12N1/19,
                                                                                                                                                                                        G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64
Survivin-like polypeptide and its DNA
                                                                                                                                               source
                                                                                            /organism='Homo
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                  Location/Qualifiers
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RESULT 12
BD248275
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DNA encoding human apopto
BD248275
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              Eukaryota;
                             Homo sapiens (human)
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                                                                                                     encoding human apoptosis
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           Metazoa; Chordata;
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Matches 792; Conserv
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Hominidae; Homo.

CE 1 (bases 1 to 1337)

RS Deng,G., Lin,J.H. and Morser,M.J.

DNA encoding human apoptosis inhibitor, protein HIAP3

AL Patent: JP 2002524039-A 1 06-AUG-2002;

SCHERING AKTIENGESELLSCHAFT

OS Homo sapiens (human)

PN JP 2002524039-A/1

PD 06-AUG-2002

FF 23-JUL-1998 US 09/127928

PI GANG DENG,JIING HUEY LIN,MICHAEL JOHN MORSER

PC C12N15/09,A61X31/7088,A61X35/76,A61X38/00,A61X38/46,A61X45/00,

PC A6189/04,A61P9/10,A61P25/14,A61P25/28,A61P31/12,A61P35/00, PC

A61837/02,

PC A61837/02,

PC G01X33/15,G01X33/50,G01X33/53,G01X33/53,G01X33/566,C12X15/00,

PC A61X37/02,A61X37/54

CC DNA encoding human apoptosis inhibitor, protein HIAP3 FH Key

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                                                      TTCCACACAGAGGCCATCAGGACAAGGTGAGGTGCTTCTTCTTGCTATGGGGGCCTGCAGAGC
                                                                                     ACCTTGTCCAGGGGCCTGCCTTCCCCGGCATGGGCTCTGAGGAGTTGCGTCTGGCCTCC
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TGGAAGCGCGGGGACGACCCCTGGACGGAGCATGCCAAGTGGTTCCCCCAGCTGTCAGTTC
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31-JUL-1998 US 09/127928
31-JUL-1998 US 09/127928
CAND DENG, JIING HUEY LIN, MICHAEL JOHN MORSER
C12N15/09, A61K31/7088, A61K35/76, A61K38/00, A61K38/46, A61K45/00,
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Location/Qualifiers
1. .1337
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AR242238.1
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DNA encoding a novel human inhibitor-of-apoptosis

Patent: US 6472172-A 1 29-OCT-2002;

Schering Aktiengesellschaft; Berlin;
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/organism="unknown"
/mol_type="genomic Di
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Guangzhou Entrepreneur Park for Overseas Chinese Scho
Baoshi Rd., GETDD, Guangzhou, Guangdong 510730, China
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1021)
Li,H., Ke,R., Wang,C.,
Direct Submission
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AY517497.1 GI:41387694
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Mammalia; Eutheria;
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                              /codon_start=1
/product="baculoviral IAP repeat-containing 7"
/product="baculoviral IAP repeat-containing 7"
/protein_id="As201729.1"
/db_xref="GI:41387695"
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DFVHSVQETHSQLLGSWDPWEEPEDAAPVAPSVPASGYPELPTPRREVQSGSAQEPGA
                                                                                                                                                                                                          /map="20q13.3"
                                                                                                                                                                                                                       /organism="Homo sapiens"
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/chromosome="20"
                                                                                                                                   note="alternatively spliced"
                                                                                                                                             gene="BIRC7"
                                                                                                                                                                     note="synonym:
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Matches 631; Conserv
Hominidae; Homo.

8 1 (bases 1 to 1168)

1 (bases 1 to 1168)

S Lin,J.-H., Deng,G., Huang,Q. and Morser,J.,

A Novel member of the inhibitor of apoptosis protein fan
Biochem. Biophys. Res. Commun. (2000) In press

E 2 (bases 1 to 1168)

S Lin,J.-H., Deng,G. and Morser,J.

Direct Submitsel (29-AUG-2000) Cardiovascular Research, Berlex
Inc., 15049 San Pablo Ave., Richmond, CA 94804, USA
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/product="inhibitor of apoptosis protein KIAP"
/protein_id="And37878,1"
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DFVHSYQETHSQLLGSWDPWEEPEDAAFVAPSVPASGYPELPTPRREVQSESAQEPGG
VSPABAQRAHWWLEPPGARDVEAQLRRLQEERTCKVCLDRAVSIVFVPCGHLVCAECA
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	80	7	თ	U1	4	Ĺ	N	ىر	Result No.
449	491	532	593	593	601	638	742	742	742	783	793	793	843	1228	1228	1228	1228	1228	Score
36.0	39.4	42.7	47.6	47.6	48.2	51.2	59.6	59.6	59.6	62.8	63.6	63.6	67.7	98.6	98.6	98.6	98.6	98.6	% Query Match
449	4810	1068	723	672	1168	858	1363	1363	1337	840	1322	1322	843	1376	1268	1268	1260	1260	Length
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Adq21877 Human sof	Adh89542 Human Liv	Aad16364 Human SBh	Aal42856 Survivin-	Aal42857 Survivin-	Adh89543 Human Liv	Adq25445 Human sof	Adt88075 Human pro	Aaa15007 cDNA enco	Aaz61210 DNA encod	Aal42858 Survivin-	Ads71344 Human liv	Acc72843 Human can	Aaf24857 Nucleotid	Aaf24856 Nucleotid	Ads71346 Human liv	Acc72844 Human can	Aea36171 Human nuc	Adh89535 Human Liv	Description

The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding Livin and that specifically hybridises with the nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The presensequence represents human livin DNA.

The present

New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.

P-PSDB; ADH89685. WPI; 2004-098436/10.

Example 13; SEQ ID NO 4; 60pp; English.

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ALIGNMENTS

ADH89535 standard; DNA; 1260

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RESULT 1
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The invention relates to a method of screening for nucleic acid molecules CC that show altered expression in a first cell sample comprising comparing CC that show altered expression in a first cell sample comprising comparing CC the gene expression profile of the sample with that of a second reference sample, where the first sample has been grown in the presence of butyrate CC or a related carbon source from which butyrate is directly or indirectly can entered, but the reference sample has not. The invention also relates to the initiation and/or progression of colorectal cancer in an animal, CC comprising providing a biological sample comprising at least one cell to be tested, contacting the sample with a ligand (preferably a hybridizing CC comprising the presence of at least one molecule in the sample, a method contacting the presence of at least one molecule in the sample, a method confidered that least one polypoptide associated with the initiation cC and/or progression of colorectal cancer in an animal comprising providing the sample comprising at least one cell to be tested, contacting the sample comprising at least one cell to be tested, contacting the sample comprising at least one cell to be tested, contacting the sample comprising at least one cell to be tested, contacting the sample with at least one one ligand that specifically binds at least one cell to be tested, contacting contacting the sample which varies by the addition, deletion or
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CC substitution of at least one amino acid residue and detecting the CC presence of the polypeptide in the sample, a method of screening for CC agents that modulate the activity of at least one polypeptide encoded by CC a gene associated with the initiation and/or progression of colorectal CC cancer comprising forming a preparation comprising at least one addition, delection or substitution and at least one agent to CC be tested and determining the activity of the agent with respect to CC activity of the polypeptide, and an antibody or its effective binding portion identified by the method, for use as a pharmaceutical. The methods are useful for screening for nucleic acid molecules that show CC altered expression in a cell sample, and for detecting a nucleic acid and CC apolypeptide respectively, that are associated with the initiation CC monitoring colorectal cancer, especially adenocarcinoma. The methods are calls useful for screening for agents that modulate the activity of at CC also useful for calcrening for agents that modulate the activity of at CC least one polypeptide encoded by a gene associated with the initiation cand/or progression of cancer, where agents identified by the methods are consulted for treating colorectal cancer. The methods could also be used to detect or monitor other conditions such as colitis, Crohn's disease or irritable bowel syndrome, as ascreening tool for fiber consumption, as call cancerous growth. This sequence represents a human nucleic acid colemntified by the screening method of the invention.
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; 2001US-0323887P.
; 2001US-035066P.
; 2002US-0355145P.
; 2002US-0355257P.
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                               BIOTECHNOLOGY INC
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CC The present invention describes an isolated nucleic acid molecule, which CC comprises the sequence of any of the genes that are up-regulated or down-CC regulated in specific cancers (e.g., about 1031 genes up-regulated in CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer CC ABR85879. ABR58799. Also described: (1) determining the presence or CC ABR85871 to ABR58799. Also described: (1) determining the presence or CC comprising a nucleic acid molecule described above; (3) a host cell CC comprising the vector; (4) an isolated polypeptide, which is encoded by CC (4); (6) specifically targeting a compound to a pathological cell in a CC drug screening assay. The nucleic acid is useful as diagnostic markers or CC diagnosting a pathology, e.g. cancer (e.g. cancer of the bone marrow, CC diagnosting a pathology, e.g. cancer (e.g. cancer of the bone marrow, CC drug screening, breast, cervix, colon/rectum, kidney, lung, ovary, CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, CC atherosclerosis and endometriosis. The nucleic acid is also useful in CC drug screening, particularly for identifying agents for treating these
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1268 BP; 204 A; 402 C; 422 G; 240 T; 0 U; 0 Other;
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SDB; ADS71347.
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e gene product, useful for eliciting an immu
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                                                                                              apoptosis inhibitor; IAP-3; cancer;
na; Alzheimer's disease; Parkinson's
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1376 BP; 233 A; 432 C; 454 G; 257 T; 0 U; 0 Other;
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Matches 843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel livin polypeptides and pathophysiological disorders melanoma cancer, Alzheimer's
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The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down-regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer related gene nucleotide sequences which encode the proteins given in ABR58521 to ABR58709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell
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                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a DNA vaccine effective for eliciting an immune response against cancer cells which comprises a DNA construct operably encoding at least one cancer-associated Inhibitor of Apoptosisfamily protein (IAP-family protein) and at least one immunoactive gene product in a pharmaceutical carrier. The invention is useful for treating cancer such as lung cancer, colorectal cancer and melanoma. The present sequence is the human livin alpha splice variant DNA.
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1322
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REFSEQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 26; SEQ ID NO 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA vaccine comprising a cancer-associated Inhibitor of Apoptosis-family protein immunoactive gene product, useful for eliciting an immu response against cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baculovirus IAP repeat domain or RING-finger domain-containing survivin-like polypeptides and encoded DNAs, applicable in diagnosis and screening compounds for treating various cancers and apoptosis abnormality.
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                                                           The present sequence encodes a human inhibitor of apoptosis protein, designated HIAP3. The protein is characterised by structural features common to the inhibitor of apoptosis protein family. The HIAP3 polypeptides can be used for the treatment of a disease state in a human patient, which is associated with inappropriate apoptosis and the patient is in need of increased levels of the polypeptide. Ribozymes, which target RNA encoding the polypeptide for treatment of inappropriate decreasing levels of the polypeptide for treatment of inappropriate apoptosis. Antisense nucleotide sequences are also useful for decreasing levels of the polypeptide. Regulation of inhibitor of apoptosis proteins neurodegenerative disorders, chronic heart failure and dysfunctional inmune response.
                                        Sequence 1337 BP;
                                                                                                                                                                               Claim 10;
                                                                                                                                                                                           New DNA encoding human inhibitor-of-apoptosis regulation of apoptosis.
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Human; proliferation and apoptosis related protein; PROAP; psoriasis; cell proliferative disorder; immunological disorder; hepatitis; reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphom; cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemia; asthma; diabetes mellitus; osteoarthritis; endometriosis;
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99US-0118559P.
99US-0172229P.
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PROAP; proliferation and apoptosis related protein; cell proliferative disorder; cancer; atherosclerosis; immunological disorder; AIDS; acquired immunodeficiency syndrome; allergy; reproductive disorder; infertility; gene therapy; cytostatic; antiarterisclerotic; immunosuppressive; anti-HIV; antiallergic; antiinfertility; gynaecological; human; gene; ss.
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                                         The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the expression in the first soft tissue sample indicates the of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
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   Dobie KW;
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Best Local Simi
Matches 651;
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an antisense oligonucleotide targeted to nucleic acid encoding Livin and that specifically hybridises with nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The property of the prop
 AAL42857;
                                       AAL42857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1168 BP;
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DB; ADH89686.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCCACACCCCAGGAGAGAGTCCCAGTCTGAAAGTGCCCAGGAGCCAGGAG
                                                                                                                                                                                                                               GAAGAACCGGAAGACGCAGCCCCTGTGGGCCCCCTCCGTCCCTTGCCTCTGGGTACCCCTGAG
                                                                                                                                                                                                                                                                                     GACTTTGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCTTGGGACCCGTGG
                                                                                                                                                                                                                                                                                                         GACTITGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCCTGGGACCCGTGG
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                                       standard; DNA;
                                                                                                                                                                                                           GAAGAACCGGAAGACGCAGCCCCTGTGGCCCCCTCCGTCCCTGCCTCTGGGTACCCTGAG
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                                       ВP
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Pred. No. 3.8e-255;
0; Mismatches 1;
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Query Match
Best Local Simi
Matches 643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises the amino acid and coding sequences of survivin-
like proteins. The survivin-like DNA and protein sequences are useful in
diagnostics and screening compounds for treating various cancers and
apoptosis abnormality, including gene therapy. The present DNA sequence
encodes a survivin-like protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 85; Page 119-120; 136pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baculovirus IAP repeat domain or RING-finger domain-containing survivin-like polypeptides and encoded DNAs, applicable in diagnosis and screening compounds for treating various cancers and apoptosis abnormality.
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P-PSDB; AAO14946.
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20-DEC-2000; 2000JP-00386809.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001; 2001WO-JP009071
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GTGCCACCCGAGCTGCTGCTGCTGCCGGCTTCTTCCACACAGGCCATCAGGACAAGGTG
                                                                                    GGCATGGGCTCTGAGGAGTTGCGTCTGGCCTTCTATGACTGGCCGCTGACTGCTGAG 465
                                                                                                                                                                         GACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGGCCCCTG
                                                                                                                                                                                                                                               GACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGGCCCCTG
                                                                                                                                                                                                                                                                                                                    GATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTAGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                CCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGGAGCCACTGGGCAGCCAGGC
                                                          GGCATGGGCTCTGAGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAG
                                                                                                                                     GATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTAGGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /partial
/product= "Survivin-like protein 4"
/note= "No stop codon is given"
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les 1;
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Qу	Ωy	Оy	Db Qy	Qy Db	Db
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Search completed: April 22, 2006, 09:46:00 Job time: 759 secs

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Result
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Maximum DB
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ALIGNMENTS

REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE RESULT 1 BU195879 LOCUS DEFINITION FEATURES COMMENT ACCESSION ORGANISM source BU195879 AGENCOURT_8050326 NIH_MGC_112 5', mRNA sequence. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP 1 (bases 1 to 884) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Homo sapiens BU195879.1 GI:22709863 EST. found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Unpublished (1999) Contact: Robert Strausberg, Ph.D. Hominidae; Homo. Eukaryota; Metazoa; Mammalia; Eutheria; BU195879 CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can fomo sapiens (human) .ate: LLCM2328 row: o column: 12 quality sequence stop: 658 Location/Qualifiers Berkeley) using ZAP-cDNA synthesis kit Superscript II RT (Life Technologies). organism="Homo sapiens' Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; 884 bp Homo mRNA sapiens linear EST 04-SEP-2002 CDNA clone IMAGE:6089315 ьe

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Hominidae; Homo.

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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                      Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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/tissue_type="melanotic melanoma, cell line"
/lab_host="DH108 (phage-resistant)"
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/clone lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
FORM; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor:
into EcoRI/XhoI sites using the following 5; adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: DCTD/DTP
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Location/Qualifiers
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Plate: LLCM2325 row:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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/lab host="DHIOB (phage-resistant)"
/clome lib="NIH MGC_112"
/clome lib="NIH MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
_corI; cDNA made by oligo-dT priming. Directionally cloned into EcorI; XhoI sites using the following 5' adaptor:
_GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2416 row: c column: 18
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5', mRNA sequence.
BQ682897
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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1 (bases 1 to 982)
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                                                                                                                                                                           e: LLCM2416 row: c column: quality sequence stop: 623.
/tissue_type="melanotic melanoma,
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/clone_lib="NIH_MGC_112"
                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6259145"
                                                                                                                                                               ocation/Qualifiers
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cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lead through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2402 row: d column: 12
High quality sequence start: 13
High quality sequence stop: 667.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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1 (bases 1 to 945)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian
Unpublished (1999)
GGACAAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGGGGGGACGA
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/tissue_type="melanotic melanoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH MGC 12"
/clone_lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT prinnig. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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|mol_type="mRNA"
|db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTp
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Biosciention information
Clone distribution: MCC clone distribute Corporation
Clone distribution: MCC clone distribution information can
County through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 912)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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AGENCOURT 8185884 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6263255
5', mRNA sequence.
BQ682378 BQ682378 GI:21795057
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Plate: LLCM2426 row: n column:
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Location/Qualifiers
                                                              Conservative
                                                                                                                                      /tissue_type="melanotic melanoma, cell line" /lab host="DH10B (phage resistant)" /clone_lib="NIH MGC_112" /clone_lib="NIH MGC_112" /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT prinning. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6263255"
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cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2347 row: c column: 07
High quality sequence start: 12
                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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AGENCOURT 7962186 NIH_MGC_112
5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                          Contact: Robert Strausberg,
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                         CD673774 621 bp mRNA linear fs04c01.y2 Human Lens cDNA (Normalized): fs Homo
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Location/Qualifiers
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/clone_lib="NIH MGC 112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/corgan: pote_1: XhoI; Site_2: Xho
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Section on Molecular Sty
National Eye Institute
6/331, NIH, Bethesda, MI
Tel: 301 402 3452
Fax: 301 496 0078
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1 (bases 1 to 621)

1 (bases 1, to 621)

Wistow, G., Bernstein, S.L., Wyatt, M.K., Behal, A., Touchman, J.W.
Bouffard, G., Smith, D. and Peterson, K.

Expressed sequence tag analysis of adult human lens for the NE
Project: over 2000 non-redundant transcripts, novel genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: graeme@helix.nih.gov
Plate: 04 row: c column: 01
Seq primor: M13RP1 reverse primer (ABI).
Location/Qualifiers
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AGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGC 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Lens"
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/lab_host="EMDH10B"
/clone_lib="Human Lens cDNA (Normalized): fs"
/clone_lib="Human Lens cDNA (Normalized): fs"
/note="Grgan: Eye; Vector: pcMVSPORT6; A human lens
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biothinylated RNA synthesis
using S96 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(C0t 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
was performed on the library at the NIH Intramural
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Pred. No. 1e-297;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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602734106F1 NIH_MGC_49 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                  http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can cound through the I.M.A.G.E. Consortium/LLNL at:
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/clone="IMAGG:485964"
/tlissue_type="melanotic melanoma, high MDR (cell line)"
/tlissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH108 (phage resistant)"
/clone_lib="MIH_MGC_49"
/clone_lib="NIH_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                         organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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602733911F1 NIH_MGC_49 Homo sapiens
                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                         1 (bases 1 to 830)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, w
Unpublished (1999)
                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                       mRNA sequence.
BG762467
BG762467.1 GI:14073120
                                                                                                                                                                                                      Homo sapiens
                                                          Contact: Robert Strausberg,
                                                                                                                                                   Hominidae; Homo.
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                                                                                                                                                                                                                     sapiens (human)
     Library Preparation: Ling Hong/Rubin Laboratory
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DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1714 row: f column: 03
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/lab_host="DH10B (phage-resistant)"
/clone_tib="NH MGC 49"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 9.9e-293;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2356 row: i column: 20
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1 (bases 1 to 956)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian
Unpublished (1999)
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BU172109 956 bp mRNA linear EST 04-SEP-2002
AGENCOURT 7954295 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6109915
5', mRNA Sequence.
BU172109
BU172109.1 GI:22686093
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                           CTAGGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTG
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/lab_host="DHIOB (phage-resistant)"
/clone_libs="NIH_MGC_112"
/clone_libs="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: xhoI; Site_2:
RCORI; cDNA made by oligo-dT priming. DIrectionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript I RT (Life Technologies). Note: this is a
NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 3.1e-290;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2331 row: e column: 07
High quality sequence stop: 580.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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AGENCOURT_8042576 NIH_MGC_112 Homo sapiens
5', mRNA sequence.
BQ877438 BQ877438 GI:22269446
EST.
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Mammalia; Eutheria;
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/tisue_type="melanotic melanoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/clone_lib="NIH_MGC_12"
/cote="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/cote="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI/CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6090222"
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                            CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2325 row: c column: 06
                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo.

1 (bases 1 to 919)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Morphy Morp
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/mol_type="mRNA"
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Tlssue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyce Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1719 row: a column: 16
High quality sequence stop: 650.
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1 (bases 1 to 652)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
ACCCGAGCTGCTGCCTGCCGCTTCTTCCACACAGGCCATCAGGACAAGGTGAGGTG
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                                                                   GGGCTCTGAGGAGTTGCGTCTGGCCTCCTTCTATGACCTGGCCGCTGACTGCTGAGGTGCC
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/lab host="DH10B (phage_resistant)"
/clone_lib="NIH MGC 49"
/clone_lib="NIH MGC 49"
/note="Organ: skin; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. DTrectionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. | "
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 5224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 603)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics (www.resgen.com).
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/note=Torgan: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Book I; Site 2: Not I; UI-E-DWO is a cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecok I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTACCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
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/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-DW0"
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Matches	583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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	178 GCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCGAGCC
	238 CAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTAGGCCTGGACACCTGCAGA 297
	298 GCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGGCCCCTGACAGAGGAGGAA 357
	358 GAGGAGGAGGCCCGGGGCCACCTTGTCCAGGGGGCCTGCCT
	418 GAGGAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAG 477
	478 CTGCTGGCTGCCGGCTTCTTCCACACACGGCCATCAGGACAAGGTGAGGTGCTTCTTC 537
	538 TGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGGACCGCCTGGACGGAGGGATGCCAAG 597
	598 TGGTTCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGAGACTTTGTCCACAGTGTG 657
	658 CAGGAGACTCACTCCCAGCTGCTGGGCTCCTGGGACCCCGTGGG 700

Search completed: April 22, 2006, 10:49:45 Job time : 5621 secs

밁 Ş 밁 á 밁 Ş 밁 Ś 밁 S 뭉 5 밁 Š В 8 멍 á 밁 Ś

Query Match Best Local Similarity

46.8%; Score 583; DB 3; Length 603; 100.0%; Pred. No. 8.8e-279;

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GenCore version (c) 1993 - 2006

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Word stage
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Maximum DB
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Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
          Issued_Patents_NA:*

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8: /cgn2_6/ptodata/1/ina/PB_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RB_COMB.seq:*
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Match
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US-09-127-928-1
US-09-949-016-66130
US-09-949-016-66131
US-09-949-016-66134
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US-09-949-016-661387
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US-09-127-928-3
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8453.595 Million cell updates/sec
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Sequence 4, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 800, App
Sequence 804, Appli
Sequence 6, Appli
Sequence 91698, A
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Sequence 1, Appli
Sequence 13691, A
Sequence 66130, A
Sequence 66140, A
Sequence 66139, A
Sequence 66134, Ap
Sequence 216, App
Sequence 216, App
Sequence 66138, A
Sequence 66138, A
Sequence 66135, A
Sequence 66135, A
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Sequence 66136, A
Sequence 66136, A
Sequence 66137, App
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	109502,	31552, A	841, App	17272, A	687, App	738, App	14376, A	12881, A	16570, A	16569, A	12788, A	16572, A	16571, A	6, Appli	10070, A	10069, A	6006, Ap	6005, Ap	194640,	194639,	01000

ALIGNMENTS

RESULT 1 US-09-949-016-1949 ; Sequence 1949, A

Patent No. 681233

Application US/09949016

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; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1949
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1949
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                               Matches 1227;
                                                                                                                                      153
                     259
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99.9%;
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; Sequence 1, Application Patent No. 6472172; GENERAL INFORMATION: APPLICANT: Deng, Gang
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; APPLICANT: MOTESEY, Michael J
; TITLE OF INVENTION: DNA Encoding a No. 64
; TITLE OF INVENTION: DVA Encoding HIAP3
; FILE REFERENCE: DNA Encoding HIAP3
; CURRENT APPLICATION NUMBER: US/09/127,928
; CURRENT ETLING DATE: 1998-07-31
; CURBENT ETLING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
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0; Mismatches
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER: 0502 ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13691
LENGTH: 8572
TYPE: DNA
ORGANISM: Human
US-09-949-016-13691
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US-09-949-016-13691
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Best Local (
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100.0%; Pred. No. 2.4e-212;
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OF DETECTION AND USES
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RESULT 4

Indels

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Gaps

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 66130
                                                                                                                                            ; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66140
                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR FILLING DATE: 2000-10-20
PRIOR FILLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

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; Patent No. 6812339
; GENERAL INFORMATION:
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GENERAL INFORMATION:
Query Match 14.0%; Score 175; DB 3; I
Best Local Similarity 100.0%; Pred. No. 2.5e-69;
Matches 175; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             SEQ ID NO 66140
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TYPE: DNA
ORGANISM: Human
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__6812339
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                                                                    Length 601;
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US-09-023-655-334
                                                                                                                      Best Local Similarity
Matches 218; Conserv
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Best Local :
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Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
                                                                                                                                                                                                                                                                                                                                           TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: KIDNNOT09
CLONE: 1419118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: HEREWITH CLASSIFICATION:
                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
              421 GAGTTGCGTCTTGGCCTTCTTTTATGACTGGCCGGCTGACTGCTGAGGTGCCACCCGAGCTG
                                                                    361 GAGGAGGCCCCGGGCCACCTTGTCCAGGGGGCCTTGCCTTCCCCGGCATGGGCTCTGAG
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                                                                                                                                                                                                                                                                l: 226 base pairs
nucleic acid
                                              GAGGAGGCCCCCGGGCCACCTTGTCCAGGGGCCTGCCTTCCCCGGCATGGGCTCTGAG 67
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CALIFORNIA
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                                                                                                                     Conservative
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                                                                                                                                                                                                                                          linear
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                                                                                                                                13.5%;
                                                                                                                                                                                                                                                                                                                                                                        PA-0001 US
                                                                                                           Score 168; DB 3; Length 226,
Pred. No. 3.9e-66;
0; Mismatches 1; Indels
0,
                                                                                                         Gaps
                   480
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Sequence 66134, Application US/09949016

Patent No. 6812339

GENNERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-0-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: PRIOR FILING DATE: 2000-09-08

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PRIOR FILING DATE: PRIOR PRIOR PRIOR FILING DATE: PRIOR PRIOR FILING DATE: PRIOR PRIOR FILING DATE: PRIOR FILING DATE: PRIOR PRI
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Best Local Similarity 100.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID 0 66139
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 66139,
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NO 66134
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100.0%; Pred. No. 1.2e-56;
ative 0; Mismatches 0;
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OF DETECTION AND USES THEREOF
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66134
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                                                                   Query Match
Best Local S
Matches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                               NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: BLADTUT04
CLONE: 1520835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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Local Similarity 100.0%; I
hes 103; Conservative 0;
                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: PALO ALTO
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                                 833
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38
                                                               ch 7.5%; Score 94; DB 3; Similarity 100.0%; Pred. No. 1.2e-3 94; Conservative 0; Mismatches
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                                                                                                                                                                                                                                           nucleic acid
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                               TGCGGCGGCTGCAGGAGGAGGACGTGCAAGGTGTGCCTGGACCGCGCCGTGTCCATCG
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                                                                                                                                                                                                                                                              200 base pairs
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Pred. No. 9.7e-37;
0; Mismatches 0;
                                                                                    1.2e-32;
                                                                                                  Length 200
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RESULT 11
US-09-949-016-66138
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US-09-023-655-387
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GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilha
TITLE OF INVENTION: EXPRESSI
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                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                            LIBRARY: BLADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 31..
STREET: 31..
CITY: PALO ALTO
CTATE: CALIFORNIA
***CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: HEREW!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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                                                                                                893 TCTTTGTGCCGTGCGGCCACCTGGTCTGTGCTGA 926
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                                                                                                                                              38 TGCGGCGGCTGCAGGAGGACGACGTGCAAGGTGTGCCTGGACCGCGCCGTGTCCATCG
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                                                                                                                                                                                                            n 7.5%; Score 94; DB 3; L
Similarity 100.0%; Pred. No. 1.2e-32;
94; Conservative 0; Mismatches 0;
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6607879
                                                                          TCTTTGTGCCGTGCGGCCACCTGGTCTGTGCTGA 131
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Sequence 66138, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOQ1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PRILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
VUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH. 601
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
UNMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 66131
LENGTH: 601
RESULT 13
US-09-949-016-66135
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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Best Local :
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Conservative (
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Best Local S
Matches 81
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-00-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOSTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 66136

LENGTH: 601
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-90-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ for Windows Version 4.0

1. ENDOWN - 66135
                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66136
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US-09-949-016-66136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66136, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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Patent No. 6812339
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Local Similarity 100.0%;
les 81; Conservative (
                                        220 CAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGAGACTTTGTCCACAGTGTGCAGGAGAC
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TCACTCCCAGCTGCTGGGCTC 686
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100.0%; Pred. No. 8.8e-27;
tive 0; Mismatches 0;
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Pred. No. 8.8e-27;
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RESULT 15
US-09-49-016-66137, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TILL OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF TILE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT PILING DATE: 2000-04-14
CURRENT PILING DATE: 2000-10-20
PRIOR APPLICATION UNMBER: 60/231,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION UNMBER: 60/231,768
PRIOR APPLICATION UNMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION UNMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SED ID NOS: 207012
SED ID
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Result
No.
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Maximum DB
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Perfect score:
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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10460.553 Million cell updates/sec
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US-10-807-897-26
US-10-807-897-26
US-10-809-882-37
US-10-723-860-8265
US-10-188-646-12
US-10-188-646-11
US-10-188-646-11
US-10-188-646-11
US-10-188-646-11
US-10-188-646-13
US-10-723-860-448
US-10-723-708-22
US-10-723-708-23
US-10-723-803-735-3
US-10-450-763-27355
US-10-450-763-27355
US-10-641-643-334
US-10-641-643-334
US-10-641-643-334
US-10-641-643-387
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Sequence 22, Appli
Sequence 27, Appli
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Sequence 334, Appli
Sequence 334, Appli
Sequence 334, Appli
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US-10-424-599-126316	US-10-425-115-39519	US-11-099-266-80	US-10-175-523-80	US-10-235-026-3	US-10-235-026-7	US-10-235-026-5	US-10-235-026-4	US-10-188-646-7	US-10-027-632-145257	US-10-027-632-145256	US-10-027-632-145255	US-10-027-632-145257	US-10-027-632-145256	US-10-027-632-145255	US-09-908-975-13132	US-10-027-632-145092	US-10-027-632-145092	US-10-027-632-14214	US-10-027-632-14213	US-10-027-632-14214	US-10-027-632-14213
Sequence 126316	Seguence 395	Sequence 80,	Sequence 80,	Sequence 3,	Sequence 7,	Sequence 5,	Sequence 4,	Sequence 7,	Sequence 145	Sequence 13132,	Sequence 145092	Sequence 14509	Sequence 14214	Sequence 14213	Sequence 14214	Sequence 14213					
316,	39519, A		Appl	Appli	Appli	Appli	Appli	Appli	145257,	145256,	145255,	145257,	145256,	145255,	32, A	092,	092,	14, A	13, A	-	13, A

ALIGNMENTS

Sequence 4, Application US/10188646
Publication No. US20040005565A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIV
FILE REFERENCE: RTS-0373
CURRENT APPLICATION NUMBER: US/10/188,646
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 4
LENGTH: 1260
TYPE: DNA
ORGANISM: H. sapiens
FEATURE: δ В δ 망 Ş 밁 δ 뮍 Ś RESULT 1 US-10-188-646-4 US-10-188-646-4 Query Match

Best Local Similarity 100.0%; P

Conservative 0; FEATURE: NAME/KEY: CDS
LOCATION: (174)...(1016) 259 153 139 273 213 199 93 79 33 19 TCTCTGGGCAGCCCTGTCCTAGGCCTGGACACCTGCAGAGCCTGGGGACCACGTGGATGGG CCACAGCCGAGCCACTGGGCCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGC GTCAGAGCCAGTGTTCCCTCCATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGA GTCAGAGCCAGTGTTCCCTCCATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGA AAGGGCCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACCTG 138 GCAGGCCTGTGCCTATCCCTGCTGTCCCCAGGGTGGGCCCCGGGGGTCAGGAGCTCCAG CCACAGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGC GGCAGGCCTGTGCCTATCCCTGCTGTCCCCAGGGTGGGCCCCGGGGGTCAGGAGCTCCAG AAGGCCCAGCTGGGCATATTCTGAGATTGGCCATCAGCCCCCATTTCTGCTGCAAACCTG TCTCTGGGCAGCCCTGTCCTAGGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGG Score 1228; Pred. No. 0; Mismatches DB 6; LIVIN EXPRESSION 0; Length 1260; Indels 0, Gaps

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272 258 212 198

152

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RESULT 2
US-10-807-897-28
Sequence 28, Application US/10807897
Publication No. US20040192631A1
GENERAL INFORMATION:
APPLICANT: Xiang, Rong
APPLICANT: Zhou, He
APPLICANT: Reisfeld, Ralph A.
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Best Local Similarity 100.0%;
Matches 1228; Conservative
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ORGANISM: homo sapi.
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FILE REFERENCE: DJB/009901/0270799 CURRENT APPLICATION NUMBER: US/10/244,586 CURRENT FILING DATE: 2002-09-16 PRIOR APPLICATION NUMBER: US/09/594,119 PRIOR APPLICATION NUMBER: US/09/594,119 PRIOR APPLICATION NUMBER: US/09/594,119 PRIOR FILING DATE: 2000-06-14 PRIOR APPLICATION NUMBER: US/09/594,119 PRIOR FILING DATE: 1999-06-15 NUMBER OF SEQ ID NOS: 12 SOFTMARE: Patentin Ver. 2.1 SEQ ID NO 1 LENGTH: 1376 TYPE DNA ORGANISM: Homo sapiens US-10-244-586-1 QUERY MATCH Best Local Similarity 100.0%; Pred. No. 0; Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1228; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1228; Conservative 0; Mismatches 12:01	RESULT 3 US-10-244-586-1 US-10-244-586-1 ; Sequence 1, Application US/10244586 ; Publication No. US20030087319A1 ; GENERAL INFORMATION: ; APPLICANT: GOMES, BRUCE C. ; APPLICANT: KASOF, GARRETT M. ; APPLICANT: PROSSER, JUDITH C. ; TITLE OF THEMETICAN, JUDITH C.	Db 1173 AGGAGGCCCTTGCTTGGCGTGGGGGATGCTTAÄCTGTÄCCTGTTTGGATGCTTCTGAAT 1232 Qy 1219 AGAAATAAAGTGGGTTTTCCCTGGAGGT 1246	1099 AGCTGGTGTCCATCCAGCACTGACCAGCCCTGATTCCCCGACCACCGCCCCAGGGTGGAGA	993 CGCGTGCGCACCTTCCTGTCCTAGGCCAGGTGCCCATGGCCAGGTGGGCTGCAGAGT 1039 GGGCTCCCTGCCCCTCTCTGCCTGTCTGGACTGTGTTCTGGGCCTGCTGAGGATGGCAG	Oy 919 TGTGCTGAGTGTGCCCCGGCCTGCAGCTGTGCCCCATCTGCAGAGCCCCCGTCCGCAGC 978	Oy 859 TGCAAGGTGTGCCTGGACCGCGCCGTGTCCATCGTCTTTGTGCCGTGCGGCCACCTGGTC 918	Qy 799 CAGGAGCCAGGAGCCAGGGATGTGGAGGCGCAGCTGCCGGCGGCTGCAGGAGGAGGAGGACG 858	Db 753 CCTGCCTCTGGGTACCCTGAGCTGCCCACACCCAGGAGAGAGGTCCAGTCTGAAAGTGCC 812
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Sequence 2, Application US/10244586

Publication No. US20030087319A1

GENERAL INFORMATION:
APPLICANT: COMES, BRUCE C.
APPLICANT: KASOF, GARRETT M.
APPLICANT: PROSSER, JUDITH C.
ITILE OF INVENTION: NOVEL PROTEIN
FILE REFERENCE: DJB/00991/0270799

CURRENT APPLICATION NUMBER: US/10/244,586

CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US/9/594,119
PRIOR APPLICATION NUMBER: 06-14
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PRIOR APPLICATION NUMBER: 06-15
INUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 843
TYPE: DNA
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Publication No. US20040192631A1
GENERAL INFORMATION:
APPLICANT: Xiang, Rong
APPLICANT: Zhou, He
APPLICANT: The Scripps Research Institute
ITILE OF INVENTION: DNA VACCINES AGAINST TUNOR GROWTH AND
ITILE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TSRI-874.1
CURRENT APPLICATION NUMBER: US/10/807,897
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/457,009
PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: 60/457,009
PRIOR FILING DATE: 2003-03-24
PRIOR FILING DATE: 2013-03-24
PRIOR FILING DATE: 2013-03-24
INUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
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FEATURE:
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RESULT 6
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Best Local S
Matches 792
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APPLICANT: Deng, Gang
APPLICANT: Lin, Jiing-Huey
APPLICANT: Worser, Michael J
TITLE OF INVENTION: DNA Encoding a No. US20030082725A1el Human Inhibitor-of-Apoptosi.
FILE REFERENCE: 50972AUSD1
CURRENT APPLICATION NUMBER: US/10/235,026
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: US 09/127,928
PRIOR APPLICATION NUMBER: US 09/127,928
PRIOR FILING DATE: 1998-07-31
NUMBER: OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENCTH: 1337
TYPE: DNA
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NAME/KEY: CDS
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US-10-839-882-37

i Sequence 37, Application US/10839882

publication No. US20040203106A1

i GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INCAPPLICANT: TANG, Y. Tom

APPLICANT: TANG, Y. Tom

APPLICANT: YUE, Henry
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: GUBCLER, Karl J.
APPLICANT: CORLEY, Neil C.
**PDTTONNT: T.M. Droefi
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                                                        APPLICANT: LAL, Précti
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUMNING, Yang
APPLICANT: JUNMING, Yang
APPLICANT: JUNMING, Yang
TITLE OF INVENTION: POLIFERATION AND APOPTOSIS RELATED PROTEINS
FILE REFERENCE: PF-0619 PCT
CURRENT APPLICATION NUMBER: US/10/839,882
CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US/09/807,452
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US/09/87,452
PRIOR APPLICATION NUMBER: US/09/87,452
PRIOR APPLICATION NUMBER: 09/175,737; unassigned; 60/118,559; 09/249,740; unassigned.
    60/154,336
PRIOR FILING DATE: 1998-10-20; 1998-10-20; 1999-02-04; 1999-04-11; 1999-04-11; 1999-04-11; 1999-04-22
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: Incyte ID No: 1520835CB1
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SOFTWARE: PERL Program
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LENGTH: 1363
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Sequence 8265, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: TIQUENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 8265
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-860-8265
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Best Local Similarity
Matches 638; Conserv
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GATGCTTCTGAATAGAAATAAAGTGGGTTTTCCCTGGA
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Sequence 12, Application US/10188646

Publication No. US20040005565A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
FILE REFERENCE: RTS-0373

CURRENT APPLICATION NUMBER: US/10/188,646

CURRENT FILING DATE: 2002-07-02

NUMBER OF SEQ ID NOS: 153

SEQ ID NO 12

LENGTH: 1168
      RESULT 10
US-10-203-708-21
Sequence 21, Application US/10203708
Sequence 21, Application US/10203708
Publication No. US20030149238A1
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; NAME/KEY: CDS
; LOCATION: (1)...(897)
US-10-188-646-12
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Best Local :
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Local Similarity 99.8%;
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RESULT 11
US-10-188-646-11
US-10-188-646-11
Sequence 11, Application US/10188646
Publication No. US20040005565A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXF
FILE REFERENCE: RTS-0373
CURRENT APPLICATION NUMBER: US/10/188,646
CURRENT FILING DATE: 2002-07-02
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US-10-203-708-21
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
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APPLICANT: SWITHKLINE BEECHAM CORPORATION
APPLICANT: SWITHKLINE BEECHAM p.l.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GES-0013
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TYPE: DNA
ORGANISM: Homo sapiens
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                                     GACTTTGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCCTGGG
                                                                                                    TGGACGGAGCATGCCAAGTGGTTCCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA
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; Pred. No. 2.1e-259;
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60 219

EXPRESSION

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RESULT 12
US-10-723-860-4697
Sequence 4697, Application US/10723860
Publication No. US20040253606A1
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PATENTIN Version 3.2
LENGTH: 449
TYPE: DNA
ORGANISM: Homo Sapiens
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ORGANISM: H. sapiens
FEATURE:
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; ORGANISM: Homo sapiens
US-10-203-708-22
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Best Local Similarity 100.0%; I Matches 449; Conservative 0;
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CURRENT APPLICATION NUMBER: US/10/203,708
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 769
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/10203708
Publication No. US20030149238A1
GENERAL INFORMATION:
APPLICANT: SWITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
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Gaps

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APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compos
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modu
FILE REFERENCE: 05882.0193.WPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR APPLICATION NUMBER: 60/429,739
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 4448
LENGTH: 676
TYPE: DNA
CORGANISM: Homo saniens
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                        CCTGCCCCTCTCTGCCCGGTTCTGGACTGTTCTGGGCCCTGCTGAGGATGGCAGAGCTGG
                                                                                                                                                      GAGTGTGCCCCCGGCCTGCAGCTGTGCCCCCATCTGCAGAGCCCCCCGTCCGCAGCCGCCGTG
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CGCACCTTCCTGTCCTAGGCCAGGTGCCATGGCCGGCCAGGTGGGCTGCAGAGTGGGCTC
                                                                                                                                 GAGTGTGCCCCGGCCTGCAGCTGTGCCCCATCTGCAGAGCCCCCGTCCGCAGCCGCGTG
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                                                                              CGCACCTTCCTGTCCTAGGCCAGGTGCCATGGCCGGCCAGGTGGGCTGCAGAGTGGGCTC
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                         CCTGCCCCTCTCTGCCTGTTCTGGACTGTGTTCTGGGCCTGCTGAGGATGGCAGAGCTGG
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSCOM
SEQ ID NO 27357
LENGTH: 3782
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (2200)...(2568)
OTHER INFORMATION: 395% homologous to Homo sapiens livin inhibitor-of-
OTHER INFORMATION: apotosis, accession number AF311388, Smith-Waterman Score=641.
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US-10-450-763-27357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (1)...(3782)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2183 GAGCCAGTGTTCCCTCCATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 GAGCCAGTGTTCCCTCCATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCAC 202
AGCCGAGCCACTGGGCAGCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTC 262
                                                                                                   TGTCCAGGGGGCCTGCCTTCCCCGGCATGGGCTCTGAGGAGTTGCGTCTGGCCTTCCT
                                                                                                                                                                           TCCTGGGCCAGCTGCGGCCCCTGACAGAGGAGGAAGAAGAGGAGGAGGGCGCCGGGGCCACCT
                                                                                                                                                                                                           TCCTGGGCCAGCTGCGGCCCCTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGACCT
                                                                                                                                                                                                                                                                                                                            TGGGCAGCCCTGTCCTAGGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGA 322
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Qy 503 ACACAG 508
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Search completed: April 22, 2006, 10:02:38
Job time: 987 secs

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Maximum DB
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seq length: 2000000000
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1: /SIDSS/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

2: /SIDSS/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

3: /SIDSS/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

4: /SIDSS/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

5: /SIDSS/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

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8: /SIDSS/ptodata/1/pubpna/USI0_NEW_PUB.seq:*

7: /SIDSS/ptodata/1/pubpna/USI0_NEW_PUB.seq:*

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17: /SIDSS/ptodata/1/pubpna/USI1_NEW_PUB.seq:*

18: /SIDSS/ptodata/1/pubpna/USI1_NEW_PUB.seq:*
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                              GenCore version 5.1.7
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14 US-11-135-855-21
14 US-11-135-855-22
8 US-10-310-914A-81037
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Sequence 81037, A
Sequence 81063, A
Sequence 81062, A
Sequence 61905, A
Sequence 61905, A
Sequence 61905, A
Sequence 61907, A
Sequence 61908, A
Sequence 61909, A
Sequence 61919, A
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-135-855-21
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CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-29
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                                                                                                                                                                                                                                                     Query Match 42.7%; Score 532; DB 14; Best Local Similarity 100.0%; Pred. No. 3e-254; Matches 532; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SMITHKLINE BEECHAM p.1.
TITLE OF INVENTION: NOVEL COMPOUNDS
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280 GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG 339
                                                                                              220 GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGGACCCCGCTCTCTGGGCAGCCCTGTCCTA 279
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GENERAL INFORMATION:

APPLICANT: SMITHKLINE BEECHAM CORPORATION

APPLICANT: SMITHKLINE BEECHAM D.1.C.

TITLE OF INVENTION: NOVEL COMPOUNDS:

FILE REFERENCE: GP50013

CURRENT ETLING DATE: 2005-05-24

PRIOR APPLICATION NUMBER: US/11/135,855

CURRENT FILING DATE: 2005-08-13

PRIOR APPLICATION NUMBER: US/10/203,708

PRIOR FILING DATE: 2007-08-13

PRIOR FILING DATE: 2001-02-14

PRIOR FILING DATE: 2001-02-14

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: 60/182,172

PRIOR APPLICATION NUMBER: 60/186,084

PRIOR PILLING DATE: 2000-02-29
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SOFTWARE: FASUSEQ for Windows Version
SEQ ID NO 22
LENGTH: 769
TYPE: DNA
CORGANIZM: Homo sapiens
US-11-135-855-22
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US-11-135-855-22
US-11-135-855-22
US-11-135-855-22
Publication No. US20050255557A1
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                                                                     GGCCTGGACACCTGGGACCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG
                                                                                              GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG
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CCCCTGACAGAGGAGGAGGAGGAGGGCGCCGGGGGCCACCTTGTCCAGGGGGCCTGCC
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US-10-310-914A-81063/c
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US-10-310-914A-81037/c

Sequence 81037, Application US/10310914A

Publication No. US20600003322A1

GENERAL INFORMATION:

APPLICANT: Shiler, Kvuzat

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

TITLE OF INVENTION: uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: Patentin version 3.3

SEQ ID NO 81037

LENGTH: 28

TYPE: RNA

ORGANISM: Human

INCLUSION SERVICED 
                                                                                                                                                                                                                                                    Sequence 8163, Application US/10310914A
Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes (
TITLE OF INVENTION: Uses thereof
FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

LENGTH: 26
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                                                                                     2.1%; Score 26; DB ilarity 100.0%; Pred. No. 0.0 Conservative 0; Mismatches
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100.0%; Pred. No.
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US-11-121-849-61904
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Sequence 61905, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
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Matches
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LENGTH: 25
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NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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CURRENT FILING DATE: 2005-05-03
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TYPE: DNA
ORGANISM: Homo sapien
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ORGANISM: Human
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; ORGANISM: Homo sapien 
US-11-121-849-61907
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US-11-121-849-61906
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; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61905
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Publication No. US20050272080A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61906
LENGTH: 25
TYPE: DNA
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Publication No. US20050272080A1
GENERAL INFORMATION:
Query Match 2.0%; Score 25;
Best Local Similarity 100.0%; Pred. No.
Matches 25; Conservative 0; Mismatch
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Best Local Similarity
Matches 25; Conserva
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Best Local Similarity 100.0%; Pred. No.
Matches 25; Conservative 0; Mismatcl
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PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator
SEQ ID NO 61305
                                                                                                                                                                                                                           TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays FILE REFERENCE: 3684.1 CURRENT FOR NUMBER: US/11/121,849 CURRENT FILING DATE: 2005-05-03 PRIOR APPLICATION NUMBER: 60/567,949 PRIOR APPLICATION NUMBER: 60/567,949 PRIOR FILING DATE: 2004-05-03 PRIOR FILING DATE: 2004-05-03 PRIOR FILING DATE: 2004-05-03
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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TITLE OF INVENTION: Methods of Genetic Analysis
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
                                                                                                                             LENGTH: 25
TYPE: DNA
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100.0%; Pred. No.
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                      DB 14;
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US-11-121-849-61910
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US-11-121-849-61909
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                         Sequence 61910, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US/11/121,849
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61909
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US-11-121-849-61908
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Best Local
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Best Local S
Matches 25
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    TITLE OF INVENTION: Methods of Genetic Analysis of
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61908
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FILE REFERENCE: 3864.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2006-03
PRIOR PILING DATE: 2005-03
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ORGANISM: Homo sapien
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hes 25; Conservative (
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Pred. No. 0.085;
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Fixed Paraffin Embedded
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61912
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, Sequence 61912, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-61911
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                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                           APPLICANT; John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION UNMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER: OF SEQ ID NOS: 673904
SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61912
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Best Local Similarity
Marches 25; Conserve
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PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61911
LENGTH: 25
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Best Local
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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION UMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
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Publication No.
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LENGTH: 25
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FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
NUMBER OF SEQ ID NOS: 673904
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25; Conserv
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US20050272080A1
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RESULT 15
US-11-121-849-61913
VS-quence 61913, Application US/11121849
Publication No. US20050272080A1
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT APPLICATION NUMBER: 005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 61913
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
Search completed: April 22, 2006, 09:51:10 Job time: 705 secs
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-Q=/abss/ABSSWEB_spool/US09762577/runat_24042006_105921_763/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2noli.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=(
-UNITS-bits -START=1 -EMD=-1 -MATRIX=01igo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000 -HOST=abss06p
-USER-US09762577_@CGN 1 7415 @cunat_24042006_105921_763 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -FGAPOP=60 -FGAPEXT=7
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REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BD167853 LOCUS COMMENT DEFINITION JOURNAL 1 (bases 1 to 840) Tanaka,H. and Kaieda,I. Tanaka,H. and Kaieda,I. Survivin-like polypeptide and its DNA Patent: WO 0233071-A 5 25-APR-2002; TAKEDA CHEMICAL INDUSTRIES LTD,HIROSHI TANAKA,ISAO KAIEDA PF 16-OCT-2001 WO 2001JP009071 PR 17-OCT-2000 JP 00P 316721,20-DEC-2000 JP 00P HIROSHI TANAKA,ISAO KAIEDA PR PR PR PR Homo sapiens (human) C12N15/09, C12N15/12, C07K14/47, C12N1/15, C12N1/19, C12N1/21, C12N5/ Hominidae; Homo. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; WO 0233071-A/5 BD167853.1 GI:27873665 BD167853 Survivin-like polypeptide and Homo sapiens (h WO 0233071-A/5 25-APR-2002 C12P21/02, C07K16/18, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, (human) 840 bp its DNA. linear PAT 17-JAN-2003 386809 ΡI PC PC

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Survivin-like polypeptide and its DNA
FH Key Location/Qualifiers
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Livin; inhibitor-of-apoptosis protein-3
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AstraZeneca AB (SE)
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Butz,K., Crnkovic-Mertens,I. and Hoppe-Seyler,F.
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Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;

Stiftung

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Patent: WO 2005054507-A 103
University of Sheffield (GB)
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WO2005054507.
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Matches:
Conservative:
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ORGANISM
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AF311388
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VERSION
                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Kasof,G.M. and Gomes,B.C.
Livin, a novel inhibitor of apoptosis protein
J. Biol. Chem. 276 (5), 3238-3246 (2001)
11024045
                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1260)
Kasof,G.M. and Gomes,B.C.
Direct Submission
Submitted (05-OCT-2000) Enabling Science and Technology,
AstraZeneca Pharmaceuticals, 1800 Concord Pike, Wilmington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
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/product="livin inhibitor-of-apotosis"
/product="livin inhibitor-of-apotosis"
/protein_id="AAG33622.1"
/db_xref="GI:11245453"
/translation="MGPKDSAKCLHRGPQPSHWAAGDGPTQERCGPRSLGSPVLGLDT
/translation="MGPKDSAKCLHRGPQPSHWAAGDGPTQERCGPRSLGSPVLGLDT
CRAWMHVDGQILGQLRFTTEEEEEEGAGATLSRGPAFPGMGSEELRLASFYDWPLTAE
VPPELLAAAGFFHTGHQDKVRCFFCYGGLQSWRRGDDDWTEHAKWFPSCQFLLRSKGR
DFVHSYQETHSQLLGSWDPWEEPEDAAPVABSVPASGYPELFTPRREYQSESAAGEFGA
                                                                                                                                        RDVEAQLRRLQEERTCKVCLDRAVSIVFVPCGHLVCAECAPGLQLCPICRAPVRSRVR
                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                           /note="inhibitor-of-apoptosis family member; and COOH-terminal RING finger domains"
                                                                                                                                                                                                                                                                                                       /gene="LIVIN"
                                                                                                                                                                                                                                                                                                                       /gene="LIVIN"
174. .1016
                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                           Length:
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                                                                                                                       Homo sapiens (
AY358835
AY358835.1 G
1 (bases 1 to 1301)
Clark, H.F., Gurney, A.L., At
Chen, J., Chow, B., Chui, C.,
                                                                                Homo sapiens (human)
Homo sapiens
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                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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clone DNA142232
                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
Abaya, E., Baker, K., Baldwin, D., ., Crowley, C., Currell, B., Deuel
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pb
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(UNQ5800) mRNA,
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              Brush, J.,
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Best Local Similarity:
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Submitted (01-AUG-2003) Department of Bioinformatics,
Location/Qualifiers
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The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
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AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp
                                                                                  PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr
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Sequence 1 from Patent WO0077201.
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AlaGlyAspGlyProThrGlnGlnArgCysGlyProArgSerLeuGlySerProValLeu
                                        ATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
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RESULT 9
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AUTHORS
TITLE
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Hominidae; Homo.

1 (bases 1 to 672)

1 Tanaka,H. and Kaieda,I.

Survivin-like polypeptide and its DNA
Patent: WO 0233071-A, 4 25-APR-2002;
TAKEDA CHEMICAL INDUSTRIES LTD,HIROSHI TANAKA,I.
OS Homo sapiens (human)
PN WO 0233071-A/4
PD 25-APR-2002
PF 16-OCT-2001 WO 2001JP009071
PR 17-OCT-2000 JP 00P 316721,20-DEC-2000 JP
HIROSHI TANAKA,ISAO KAIEDA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
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                                           GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu
                                                                                                                                                                                                                                                                         LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro
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                                                                                                     GAAGAACCGGAAGACGCAGCCCCTGTGGCCCCCCCTCCGTCCCTGCCTCTGGGTACCCTGAG
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Location/Qualifiers
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US-09-762-577B-12 (1-309) x BD185364 (1-672)
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1 (bases 1 to 672)

1 TANAKA, H. and Kaieda, I.

Survivin-like polypeptide and its DNA
PAREDA CHEMICAL INDUSTRIES LTD

OS Homo sapiens (human)

PN JP 2002355062-A, 4

PD 10-DEC-2002

PP 16-OCT-2001 JP 2001318533

PI HIROSHI TANAKA, ISAO KAIEDA

PC C12N15/09, A61K31/7088, A61K38/55, A61K

PC 00, A61P35/00,

PC 00, A61P35/00, C07K14/82, C07K16

PC C12N15/10, C12P21/02, C12Q1/02, C12Q1/68

PC C12N33/53, GO1N33/566, GO1N33/574, C12N

CG Survivin-like polypeptide and its DN

FH Key

FT source

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PT SOURCE

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PT 1-C121/2/ (JC7ganism='Homo sapi
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JP 2002355062-A/4
                                                        AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp
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Survivin-like polypeptide and its DNA
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/mol_type="genomic DNA"
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Survivin-like polypeptide and its DNA
Patent: WO 0233071-A 3 25-APR-2002;
TAKEDA CHEMICAL INDUSTRIES LTD, HIROSHI TANAKA, ISAO KAIEDA
OS Homo sapiens (human)
PN WO 0233071-A/3
PD 25-APR-2002
PF 16-0CT-2001 WO 2001JP009071
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     ATGGGGCCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
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16-0CT-2001 WO 2001JP009071
17-0CT-2000 JP 00P 316721,20-DEC-2000 JP 00P
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/db_xref="taxon:9606"
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Query Match: DB:

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Hominidae; Homo.

1 (bases 1 to 723)

Tanaka, H. and Kaieda, I.

Survivin-like polypeptide and its DNA
Patent: JP 2002355062-A 3 10-DEC-2002;

TAKEDA CHEMICAL INDUSTRIES LTD
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BD185363
BD185363.1 GI:31877563
JP 2002355062-A/3.
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                  Homo sapiens (human)
JP 200235502-A/3
10-DEC-2002
16-OCT-2001 JP 2001318533
HIROSHI TANAKA, ISAO KAIEDA
C12N15/09, A61K31/7088, A61K38/55, A61K39/395, A61K39/395, A61K48/00, A61P35/00,
                                                 G01N33/53,G01N33/566,G01N33/574,C12N15/00,C12N5/00,A61K37/64
Survivin-like polypeptide and its DNA
                                                                                                  C12N5/10, C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50,
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/organism='Homo sapiens
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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REFERENCE AUTHORS TITLE

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PF 16-OC
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PC C12NJ
PC A61PP
C12NJ/21,
PC C12NS
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SOURCE ORGANISM

Homo sapiens Homo sapiens (human)

KEYWORDS

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1 (bases 1 to 1168)

Lin,J.-H., Deng,G., Huang,Q. and Morser,J.

A Novel member of the inhibitor of apoptosis protein Biochem. Biophys. Res. Commun. (2000) In press 2 (bases 1 to 1168)

Lin,J.-H., Deng,G. and Morser,J.

Submitted (29-AUG-2000) Cardiovascular Research, Berl Tengen 1 to 129-AUG-2000) Cardiovascular Research, Berl
                    LysValArgCysPhePheCysTyrGlyGlyLeuGlnSarTrpLysArgGlyAspAspPro 140
                                                                                                                                                                                                                                                                                                                                                                                                               MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla
AAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCC
                                                                                         AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
                                                                                                                                                   PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr
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/codon_start=1
/product="inhibitor of apoptosis protein KIAP"
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VSPAEAQRAHWVLEPPGARDVEAQLRRLQEERTCKVCLDRAVSIVFVPCGHLVCAECA
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721. .867
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/chromosome="20"
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mol_type="mRNA"
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LIVIN-SPECIFIC siRNAS FOR THE TREATMENT OF THERAPY-RESISTANT
Patent: WO 2004091388-A 10 28-OCT-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 from Patent CQ896990 CQ896990.1 GI:55581832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                      ProLeuThrGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla
                                                                                                                                                            GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
                                                                                                                                                                                                                      AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu
                                                                                                                                                                                                                                                          ATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
                                                 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
                                                                                  CCCCTGACAGAGGAAGAGGAGGAGGAGGCGCCGGGGCCACCTTGTCCAGGGGGCCTGCC
                                                                                                                                                                                                  GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTA
                                                                                                                                                                                                                                                                            MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla
                                                                                                                                            GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG
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/mol_type="unassigned DN/
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Alteschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerth, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
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                                                                                                                                                                                                                                                                                 Direct Submission

Submitted (17-SEP-2001) National Institutes of Health, Mammalian Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Cancer G
                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ă
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BC014475.1 GI:15680240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                             NIH-MGC Project URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12477932
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Library Preparation: Rubin Laboratory
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                        http://mgc.nci.nih.gov
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: f Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536419. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Genome Sequence Centre BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
ProLeuThrGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
                                                                                                                                                                      GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTA
                                                                                                                                                                                                                                                                 ATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
                                                                                                                                                                                                                                                                                                                MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
                                                                                                GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
                                                                      GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/protein_id="AAH14475.1"
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DFVHSVQETHSQLLGSWDPWEEPEDAAPVAPSVPASGYPELPTPRREVQSESAQEPGG
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149. .1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MGC:23131 IMAGE:4859588"
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/clone Iib="NIH MGC 49"
/lab_host="DH10B-R"
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db_xref="GeneID:79444"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="BIRC7"
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AAAGTGCCCAGGAGCCAGGA 799	CTGCCCACACCCAGGAGAGAGGTCCAGTCTGAA	749	Db
luserAlaGlnGluproGly 217	LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGly	201	Ş
CCTCCGTCCCTGCCTCTGGGTACCCTGAG 748	GAAGAACCGGAAGACGCACCCTGTGGCCCCCTCCGTCCCTTGGGTACCCTGAG	689	B
roSerValProAlaSerGlyTyrProGlu 200	GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu	181	Ş
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erGlnLeuLeuGlySerTrpAspBroTrp 180	AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp	161	ş
GTCAGTTCCTGCTCCGGTCAAAAGGAAGA 628	TGGACGGAGCATGCCAAGTTGCTCCCAGCTGTCAGTTCCTCCGGTCAAAAGGAAGA	569	рb
ysGlnPheLeuLeuArgSerLysGlyArg 160	TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg	141	Ş
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llaGlyPhePheHisThrGlyHisGlnAsp 120	AlaGluValProProGluLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAs	101	δÃ
TGGCCTCCTTCTATGACTGGCCGCTGACT 448	TTCCCCGGCATGGGCTCTGAGGAGTTGCGTCTGGCCTCTTCTATGACTGGCCGCTGACT	389	DЬ
LeuAlaSerPheTyrAspTrpProLeuThr 100	PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr	81	ş

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-Q-/abss/ABSSWEB_spool/US09762577/runat 24042006 105917 692/app query.fasta_1
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -FGAPOP=60 -FGAPO
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                                                                                                                                                                                                                                                                     Score
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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ALIGNMENTS

RESULT 1 AAL42858

AAL42858 standard; DNA; 840 BP

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Survivin-like protein; diagnosis; screening; cancer; gene; ds; apoptosis abnormality; gene therapy.
       16-OCT-2001; 2001WO-JP009071
                        25-APR-2002.
                                         WO200233071-A1.
                                                                                                                   Unidentified
                                                                                                                                                           Survivin-like protein coding sequence 5.
                                                                                                                                                                             05-AUG-2002
                                                                                                                                                                                              AAL42858;
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                                                        /product= "Survivin-like protein
/note= "No stop codon is given"
                                                                                                  Location/Qualifiers
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequences of survivin-
like proteins. The survivin-like DNA and protein sequences are useful in
diagnostics and screening compounds for treating various cancers and
apoptosis abnormality, including gene therapy. The present DNA sequence
encodes a survivin-like protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baculovirus IAP repeat domain or RING-finger domain-containing survivin-
like polypeptides and encoded DNAs, applicable in diagnosis and screenin
compounds for treating various cancers and apoptosis abnormality.
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P-PSDB; AAO14947.
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                  GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu
                                                                    AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp
                                                                                                     TGGACGGAGCATGCCAAGTGGTTCCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA
                                                                                                                       TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
                                                                                                                                                         AAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCC
                                                                                                                                                                           LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro
                                                                                                                                                                                                                              AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp
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2000JP-00386809
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Conservative:
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RESULT 2
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KW mela
XX Homc
FH Key
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                                     The present sequence encodes a human polypeptide, designated livin. Livin is an inhibitor of apoptosis protein 3 (IAP-3). Livin is present in certain cancer cell lines and prevents apoptosis. The livin polypeptide is useful for identifying compounds that inhibit and modulate livin function and activity. Such compounds that inhibit and medulate livin dysfunctional apoptosis condition. Livin polypeptides are useful as a source of probes and primers, and in gene therapy. Livin polypeptides and polymucleotides, their inhibitors and modulators are useful for treating pathophysiological disorders related to apoptosis, cancers, particularly melanoma cancer, Alzheimer's disease and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                    Novel livin polypeptides and polynucleotides useful for treating pathophysiological disorders related to apoptosis, cancers, particularly melanoma cancer, Alzheimer's disease and Parkinson's disease e.g. by gene
                                                                                                                                                                                                                                                                                                                                                        Claim
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)B; AAB31478.
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New antisense oligonucleotide, having a sequence targeted acid encoding Livin, useful for preparing a composition for hyperproliferative disorder or aberrant apoptosis.
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                    ed to a nucleic for treating
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The invention relates to an antisense oligonucleotide targeted to nucleic acid encoding Livin and that specifically hybridises with nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The presquence represents human livin DNA.

BP; 201 A; 398 Ç 421 ٠<u>.</u> 240 τ, 0 U; 0 Other;

Percent Similarity:
Best Local Similarity:
Query Match: (1-309) x ADH89535 3.62e-257 280.00 100.0% 100.0% 90.6% (1-1260)Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1260 280 0 0

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GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
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                                         MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla
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                                                                                                                                                               Disclosure; Page 143; 266pp; English.
                                                                                                                                                                                                                                 Screening for nucleic acid molecules exhibiting altered expression in cells grown in the presence of butyrate, and detection of the nucleic acid molecules or the encoded polypeptides in diagnosing colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-DEC-2004; 2004WO-GB005078.
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cc a method of detecting at least one nucleic acid molecule associated with cc comprising providing a biological sample comprising at least one cell to comprising providing a biological sample comprising at least one cell to comprising a coid molecule) which binds to at least one nucleic acid and presence of at least one molecule in the sample, a method cc and/or progression of colorectal cancer in an animal comprising providing the sample with at least one polypeptide associated with the initiation cc the sample with at least one polypeptide associated with the initiation cc the sample with at least one ligand that specifically binds at least one can amino acid sequence which varies by the addition, deletion or comprising providing the presence of the polypeptide in the sample, a method of screening for cancer comprising forming a preparation comprising and excepting the presence of the polypeptide in the sample, a method of screening for cancer comprising forming a preparation comprising at least one associated with the initiation and/or progression of colorectal cacid or a variant polypeptide emcoded by a pulleic acid or a variant polypeptide comprising cancer and detecting the polypeptide, and an antibody or itself exception of colorectal cacid or a variant polypeptide comprising capture of the agent with respect to comprise associated and detecrmining the activity of the agent with respect to cativity of the method, for use as a pharmaceutical. The methods are useful for screening for nucleic acid molecules that show a polypeptide respectively, that are associated with the initiation or substitution and are useful for detecting or molitoring colorectal cancer, where agents that modulate the activity of also useful for screening for mucleic acid molecules that show a polypeptide respectively, that are associated with the initiation or also useful for screening for molitoring and provided are useful for detecting or analyce provided and captured with the initiation or analyce provided and captured with the i

1260 BP; 201 A; 398 C; 421 G; 240 T; 0 U; 0 Other;

IIS-09-763 E775 15 /1 350	Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Query Match: DB:
	3.62e-257 280.00 100.0% 100.0% 100.0% 14
	Length: Matches: Conservative: Mismatches: Indels: Gaps:
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US-09-762-577B-12 (1-309) x AEA36171 (1-1260)

Ş	Д	MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20
Db	174	
γQ	21	AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
Db	234	
8	41	GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
Db	294	
γQ	61	ProLeuThrGluGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
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γQ	81	
Db	414	
γQ	101	AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
Db	474	GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCCGGCTTCTTCCACACAGGCCATCAGGAC 533

invention relates to

invention relates to a method of screening for nucleic acid molecules show altered expression in a first cell sample comprising comparing lene expression profile of the sample with that of a second reference le, where the first sample has been grown in the presence of butyrate crelated carbon source from which butyrate is directly or indirectly have the reference sample has not. The invention also relates to

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RESULT 5
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20-SEP-2001;
13-NOV-2001;
08-FEB-2002;
08-FEB-2002;
12-APR-2002;
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Zlotnik
                                      New genes that are up-regulated or down-regulated in cancers, u markers for diagnosing e.g. cancer, ischemia or heart diseases, therapeutic targets for screening drugs for treating these dise
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Claim 8; Page 725-726; 767pp; English.
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P-PSDB; ABR58693.
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; 2001US-0323887P.
; 2001US-0350687P.
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DB:
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related gene nucleotide sequences which encode the protestins given in ABRS821 to ABRS8709. Also described: (1) determining the presence or absence of a pathological cell in a patient; (2) an expression vector comprising a nucleic acid molecule described above; (3) a host cell comprising the vector; (4) an isolated polypeptide, which is encoded by the nucleic acid; (5) an antibody that specifically binds the polypeptide of (4); (6) specifically targeting a compound to a pathological cell in a patient by administering to the patient the antibody above; and (7) a drug screening assay. The nucleic acid is useful as diagnostic markers or therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometriosis. The nucleic acid is also useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated nucleic acid molecule, which comprises the sequence of any of the genes that are up-regulated or down regulated in specific cancers (e.g. about 1031 genes up-regulated in acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
                                                                                       screening, particularly for identifying agents for treating these
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Sequence 1268 BP; 204 A; 402 <u>ე</u> 422 G; 240 ij 0 U; 0 Other,

Alignment

No.:

3.64e-257 280.00 100.0% 100.0% 90.6%

Length:
Matches:
Conservative:
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                                                                     The present invention relates to a DNA vaccine effective for eliciting an immune response against cancer cells which comprises a DNA construct operably encoding at least one cancer-associated Inhibitor of Apoptosis-family protein (IAP-family protein) and at least one immunoactive gene product in a pharmaceutical carrier. The invention is useful for treating cancer such as lung cancer, colorectal cancer and melanoma. The present sequence is the human livin beta splice variant DNA.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA vaccine comprising a cancer-associated Inhibitor of Apoptosis-family protein immunoactive gene product, useful for eliciting an immu response against cancer.
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Best Local Similarity:
Query Match:
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/note= "No stop codon is given"
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like polypeptides and encoded DNAs, applicable in diagnosis and screening
compounds for treating various cancers and apoptosis abnormality.
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                                                                                           GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu
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                                                                                                                                                                                                                                                                                                          Baculovirus IAP repeat domain or RING-finger domain-containing survivin-like polypeptides and encoded DNAs, applicable in diagnosis and screening compounds for treating various cancers and apoptosis abnormality.
                                                                                                                                                                                                                                                                                          Claim 5;
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20-DEC-2000;
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GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
                                            AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu
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                                                                      ATGGGGCCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
                                                                                                                                                                                                              723
                                                                                                                                                                                                                                                                                        Page 117-118; 136pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA;
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/product= "Survivin-like
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The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding Livin and that specifically hybridises with to nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for
                                                                                                                        New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.
                                                                                                                                                                                                                                                                                                                            02-JUL-2002;
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Best Local Similarity:
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                      Human; cancer;
heart disease;
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                                  diagnosis; screening; modulator; leukaemia;
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Best Local Similarity:
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08-FEB-2002;
08-FEB-2002;
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; 2001US-035666P.
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; 2002US-0372246P.
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New DNA vaccine comprising a family protein immunoactive
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a cancer-associated Inhibitor of Apoptosis-e gene product, useful for eliciting an immu

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                                                                                AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu
                                                                                                                            ATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
                                                                                                                                             MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla
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GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG
                                                             GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTA
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11-FEB-1999;
22-APR-1999;
                        Tang YT,
Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; proliferation and apoptosis related protein; PROAP; psoriasis; cell proliferative disorder; immunological disorder; hepatitis; reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma; cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemia; asthma; diabetes mellitus; osteoarthritis; endometriosis; uterine fibroid; menstrual cycle; ss.
                                                                                                                                                                                                                                                                                                              27-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding a human proliferation and apoptosis related
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                   Baughn
              H, Hillman JL, (
aughn MR, Yang J,
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The present sequence encodes a human proliferation and apoptosis related protein (PROAP). The polypeptides and polynucleotides can be used for the diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders. Disorders associated with decreased expression or activity of include arteriosclerosis, cirrhosis, hepatitis, psoriasis, melanoma, lymphoma and canneers of the breast, brain and prostate, acquired immune deficiency syndrome (AIDS), allergies, anaemia, asthma, diabetes mellitus, osteoarthritis, endometriosis, uterine fibroids and disruptions of the menstrual cycle. Antibodies against proap can be use in diagnosis of disorders characterized by PROAP e.g. in ELISA (enzyme linked immunosorbent assays) and the polynucleotides may be used to detect and quantify gene expression in biopsied tissues. These techniques can also be used to monitor regulation of PROAP levels during
                                           therapeutic intervention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human proliferation and apoptosis related protein polypeptides used for diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 121; 128pp; English.
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P-PSDB; AAY84907.
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Alignment S Pred. No.: Query Match: DB: Percent Similarity: Best Local Similarity: 5.1e-197 217.00 100.0% 100.0% 70.2% Length:
Matches:
Conservative:
Mismatches:
Indels: 1363 217 0 0

Sequence

ВP;

228 A; 428

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U; 0 Other;

Scores: 1363

US-09-762-577B-12 (1-309)x AAA15007

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694	TGGACGGAGCATGCCAAGTTGGTTCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA ASDPheValHisSerValGlnGlnThrHisSerGlnLanLenGlySerTunksnnrcTun	635 161	& B
160	TrpThrGluHisAlaLySTrpPheProSerCysInPheLeuLeuArgSerLySGlyArg	141	δ
140	ysValhxgCyshhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro	121 575	유 성
574	GCTGAGGTGCCACCCGAGCTGCTGCTGCTGCCGGCTTCTTCCACACAGGCCATCAGGAC	515	Db
120	AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp	101	Ş
514		455	Дb
100	PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr	81	Ş
454		395	ర్థ
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334		275	ర్జ
40	AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu	21	Ş
	ATGGGGCCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCAGCC	215	뭥
20	1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla		Ş

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                                                                    The present invention relates to the human proliferation and apoptosis related protein (PROAP) and its encoding nucleic acid. The invention is useful for diagnosing, preventing or treating disorders associated with altered expression or activity of human PROAP, such as cell proliferative (e.g. cancer or atherosclerosis), immunological (e.g. acquired immunodeficiency syndrome (AIDS) or allergies) or reproductive (e.g. infertility) disorders. The invention is also be used in screening for drugs that may be used for treating or preventing the disorders mentioned above and in gene therapy. The present sequence is the human PROAP-18
                                                                                                                                                                                                                                                                                                                                                                                   New human proliferation and apoptosis related proteins and polynucleotides for diagnosing, preventing or treating disorders associated with aberrant protein expression, e.g. cancer, AIDS, atherosclerosis or infertility.
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Azimzai
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19-OCT-1999;
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P-PSDB; ADT88056.
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(PROAP)-18"
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Qγ	B &	D QY	ДУ	Qy Db	Qу Db	Qy Db	Qy Db	Qу Db	Qy Db	Qy Db	US-09-762	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:
201 LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGly 217	CONTROL CONT	61 AspPhoValHisSerValGinGluThrHisSerGlnLeuLeuGlySerTrpAspproTrp 18 61	141 TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160	121 LysValargCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140	101 AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120	81 PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100	61 ProLeuThrGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80	41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60	21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40	1 MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla 20 	-577B-12 (1-309) x ADT88075 (1-1363)	nment Scores: . No: ;

Search completed: April 24, 2006, 11:11:43 Job time: 742 secs

Sequence protein

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-MODEL-frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US09762577/runat_24042006_105924_898/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US09762577/runat_24042006_105924_898/app_query.fasta_1
-DB=EST_QFWY=fastap_SUFFIX=p2noli.rst_-MINWATCH=0.1 -LOOPCL=0_-LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MATRIX=000000000 -15924_898 -NCPU=6 -ICPU=3
-USER=US09762577_@CGN_1_1_5315_@runat_24042006_105924_898 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=60 -XGAPEXT=60 -FGAPEXT=7
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1. 884 /organism="Homo sapiens"	Plate: LLCM2328 row: o column: 12 High quality sequence stop: 658. Location/Qualifiers	<pre>found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</pre>	DNA Sequencing by: Agencourt Bioscience Corporation can be Clone distribution: MGC clone distribution information can be	CDNA LIDRARY Preparation: Kubin Laboratory	Tissue Procurement: DCTD/DTP	Email: cgapbs-r@mail.nih.gov	Contact: Robert Strausberg Dh D	National Institutes of Health, Mammalian Gene Collection (MGC)	C http://mgc.nci.nih.gov/.	(bases 1 to 884)		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	apiens	Homo sapiens (human)		BU195879.1 GI:22709863	79	, mRNA sequence.	AGENCOURT_8050326 NIH MGC_112 Homo sapiens cDNA clone IMAGE:6089315	79 884 bp mRNA linear EST 04-SEP-2002		

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/note="Ozgan: poTB7; Site_1: xhoI; Site_2: xhoI
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RESULT 2 BQ682827 LOCUS

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Best Local Similarity:
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Tissue Procurement: DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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             PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
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GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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BQ682897
BQ682897.1 GI:21795576
EST.
                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLCM216 row: c column: 18
High quality sequence stop: 623.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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EcoRI; cDAN made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                                                                                           /tissue type="melanotic melanoma, cell line"
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Hominidae; Homo.

1 (bases 1 to 621)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Behal,A., Touchman,J.W.,
Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of adult human lens for the NEIBank
Project: over 2000 non-redundant transcripts, novel genes and
splice variants
splice variants
Mol. Vis. 8 (4), 171-184 (2002)
                                                                                                                                                                                                                                                           CD673774
CD673774.1
                                                                                                                                                                                                                                                                                         fs04c01.y2 Human Lens cDNA (Normalized): fs Homo fs04c01.5', mRNA sequence.
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProLeuThrGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
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COMMENT

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           363
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                                                                              303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 04 row: c column: 01 Seq primer: M13RP1 reverse primer
                                                                                                                                                                   GluLeuArgLeuAlaSerPheTyrAspTrpProLeuThrAlaGluValProProGluLeu 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: graeme@helix.nih.gov
Plate: 04 row: c column:
TATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCCTGGACGGAGCATGCCAAGTGG
                          TyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspProTrpThrGluHisAlaLysTrp 147
                                                                                              LeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAspLySValArgCysPhePheCys 127
                                                                                                                                            GAGTTGCGTCTGGCCTCCTTCTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGCTG
                                                                                                                                                                                                                   GAGGAGGGCGCCACCTTGTCCAGGGGGCCTGCCTTCCCCGGCATGGGCTCTGAG
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                                                                                                                                                                                                                                                                                                                                                               GAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTAGGCCTGGACACCTGCAGAGCC
                                                                                                                                                                                                                                                                                                                                                                                        GluArgCysGlyProArgSerLeuGlySerProValLeuGlyLeuAspThrCysArgAla 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysCysLeuHisArgGlyProGlnProSerHisTrpAlaAlaGlyAspGlyProThrGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Human Lens cDNA (Normalized): fg"
/note="Organ: Eye; Vector: pcMVSPORT6; A human lens
library (by) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(COt 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/se-circles were
was performed on the library at the NIH Intramural
Sequencing Center(NISC)."
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/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fs04c01"
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               Percent Similarity:
Best Local Similarity:
Query Match:
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMM2402 row: d column: 12
High quality sequence start: 13
High quality sequence stop: 667.
Location/Qualifiers
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1 (bases 1 to 945)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

Tissue Procurement: DCTD/DTP
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5', mRNA sequence.
BU180020
BU180020 GI:22694004
EST.
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/clone_lib="NIH_MGC_112"
/clone_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript IRT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6253787"
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Mismatches: Indels: Gaps:

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AUTHORS
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2325 row: a column: 17
                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
                                                                                                                                                  1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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BQ892691.1 GI:22284705
EST.
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Mammalia; Eutheria;
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Homo sapiens
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/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site_2:
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. DTrectionally clone;
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:6087832"
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/lab_host="DH108 (phage-resistant)"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2501 row: a column: 19
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Unpublished (1999)
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AGENCOURT 8712345 NIH_MGC_112
5', mRNA fequence.
BU150825
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Tissue Procurement: DCTD/DTP
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                            GluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAlaPheProGlyMet
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GGCTCTGAGGAGTTGCGTCTGGCCTCCTTCTATGACTGCCGCTGACTGCTGAGGTGCCA
                         GlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThrAlaGluValPro 104
                                                                                GAGGAAGA
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                                                                                                                                                                                                                                               ProThrGlnGluArgCyeGlyProArgSerLeuGlySerProValLeuGlyLeuAspThr 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="melanotic melanoma, cell line"
/lab host="NHHOB (phage-resistant)"
/clone_lib="NIH_MGC_112"
/clone_lib="NIH_MGC_12"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/KhoI sites using the following 5; adaptor:
GCACCAGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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mol_type="mRNA"
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1749 row: g column: 06
High quality sequence stop: 740.
Iocation/Qualifiers
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1 (bases 1 to 740)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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/lab host="DH10B (phage-resistant)"
/clone_lib="NH10B (phage-resistant)"
/clone_lib="NH10B (phage-resistant)"
/clone_lib="NH1 MGC_49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECGRI; CDNA made by oligo-dT priming. DTrectionally cToned
into EcGRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using_ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. |"
                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
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                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                               mRNA sequence. - - BG770075
BG770075.1 GI:14080728
EST.
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602745008F1 NIH_MGC_49 Homo sapiens
                                                                                                                                           Homo sapiens
                                                                                                                                                    Homo sapiens (human)
                                                                                                           Hominidae; Homo.
  cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                            GluGluProGluAspAlaAla 187
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                             TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_49"
/clone_lib="NIH MGC_49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; CDNA made by oligo-dT priming. DIrectionally cloned into ECORIXhoI sites using the following 5 adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"
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Plate: LLCM2327 row: n column: 03
High quality sequence start: 22
High quality sequence stop: 574.
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Tissue Procurement: DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/lab host="DH10B (phage-resistant)"
/clone lib="NH10B (phage-resistant)"
/clone lib="NH MGC 112"
/note="Organ: skin; "Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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/mol_type="mRNA"
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164 HisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrpGluGluPro 183
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Plate: LLCM2356 row: 1 column: 20
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Tissue Procurement: DCTD/DTP
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1 (Dases 1 to 956)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/mol_type="mrNA"
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/db_xref="taxon:9606"
/clone="IMAQE:6109915"
/tissue_type="melanotic melanoma, cell line"
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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AGENCOURT 7962186 NIH MGC_112 Homo
5', mRNA sequence.
BU188703
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
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Plate: LLCM2347 row: c column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glu 181
                                                                                                                                                                                                                      LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro
                                                                                                                                                                                                                                                                                                   AlaGluValProProGluLeuLeuAlaAlaGlyPhePheHisThrGlyHisGlnAsp
                                         GACTTTGTCCACAGTGTGCAAGAGACTCACTCCCAGCTGCTGGGCTCCTGGGACCCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCTGACAGAGGAAGAAGAGGAGGAGGGCCCCGGGGCCACCTTGTCCAGGGGGCCTGCC
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                                                                AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
                                                                                                                                              TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
                                                                                                                                                                                                                                                                              PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAapTrpProLeuThr
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                                                                                                                   TGGACGGAGCATGCCAAGTGGTTCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol type="make" / /molte="NAGE:6106302" //molte="NAGE:6106302" /molte="NAGE:6106302" /molte="NAGE:6106302
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Conservative:
Mismatches:
Indels:
Gaps:
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744

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US-09-762-577B-12 (1-309) x BM696272 (1-603)
                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                      Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COORDINATED LABORATORY FOR COMPUTATIONAL GENOMICS UNIVERSITY OF TOWA 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242 Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8889548
Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM696272 603 bp mRNA linear EST 28-FEB-2002 UI-E-DW0-agl-c-11-0-UI.r1 UI-E-DW0 Homo sapiens cDNA clone UI-E-DW0-agl-c-11-0-UI 5', mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                    /note=Torgan: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-B-DW0 is a cDNA library containing the following tissue(s): lens. The library was constructed according bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into DT73-Pac vector. The first-strand cDNA contains a library tag sequence that is sequence tag for this library is CGATTRAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-E-DWO-agl-c-11-0-UI"
/tissue_type="lens"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type≈"mRNA"
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Jennon,G. and Soares,M.B.
and subtraction: two approaches to facilitate gene
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e_lib="UI-E-DW0"
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161 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp
                                                                                                                                                                                                                   Email: cgapbs r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2331 row: e column: 07

High quality sequence stop: 580.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae; Homo.

1 (bases 1 to 870)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg 60
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5', mRNA sequence.
BQ877438
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/db xref="taxon:9606"
/clone="IMAGE:6090222"
                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                      organism="Homo sapiens"
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ORIGIN

Pred. No.: Alignment

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Percent Similarity:
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Query Match:
DB:
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1 (bases 1 to 912)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                            Hominidae; Homo.
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Conservative:
Mismatches:
Indels:
Gaps:
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sapiens
                   Gene Collection
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REFERENCE AUTHORS TITLE JOURNAL

RESULT 15 BQ682378 LOCUS

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ACCESSION VERSION

KEYWORDS

SOURCE ORGANISM

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CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCN2426 row: n column: 24

High quality sequence stop: 609.

Location/Qualifiers
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                                                                                                                                            LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
                                                                                                                                                                                                                     AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp
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                                                                TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
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/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/clone_lib="NIH_MGC_112"
/note="Toggan: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. DTrectionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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Db 544 GACTTTOTCCACAGTGCACGGACTCACTCCCAGCTGCTCCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCCAGTGCTCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTA

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Word Size
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=Abss/ABSSWEB spool/US09762577/runat 24042006 105928 1006/app query.fasta 1
-Q=Abss/ABSSWEB spool/US09762577/runat 24042006 105928 1006/app query.fasta 1
-DB=Issued patents NA -QFWT=fastap -SUFFIX=p2nol1.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
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-UIST=45 -DOCALIGN=200 -THR SCORES=00 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs006h
-USER=US09762577 @CGN 1 1 143 @runat 24042006 105928 1006 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -FGAPOP=60 -FGAPDEXT=7
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PE_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Ygapop 60.0,
Fgapop 60.0,
Delop 60.0,
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Match Length
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         90.6
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d by analysis of the total score distribution.
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1337
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Fgapext 7.0
Delext 60.0
  US-09-949-016-1949

US-09-127-928-1

US-09-949-016-166130

US-09-949-016-66140

US-09-949-016-66140

US-09-949-016-66134

US-09-023-655-334

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Sequence 1949, Ap
Sequence 1, Appli
Sequence 13691, A
Sequence 66130, A
Sequence 66130, A
Sequence 66139, A
Sequence 334, App
Sequence 66134, A
Sequence 216, App
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ω	w	N	σ	w	w	w	Φ	w	w	w	σ	ω	w	W	W	ω	w	ω	N	w	ω	ω	w	W	W	w	9	ω	W	w	ω	w	ω	w	ω
US-09-212-971-13	-09-814-9	-09-205-1	860	32-286-	89-366-1	08-569-74	T-US96-12860-	10-232-286-	9-689-3	08-569-749-	T-US96-12860	10-232-	-09-689-366-	-08-569-749-	-09-201-932-	US-09-672-717-222	-09-	-09-201-93	US-08-511-485-7	-09-023-655-	-09-016-434-1	-09-201-932-4	-09-672-717-2	-09-011-356-4	9-201-936-	9-023-655-49	T-US95-	9-949-016-176	US-09-949-016-21029	-09-949-016-66	-09-949-016-6613	-09-949-016-6613	-09-949-016-6613	-09-949-016-6613	-09-023-655-3
e 13,	æ	equence 1,	e 13,	e 13,	e 13,	e 13,	ω v	e u	e u	equence 3, Appl	equence 1, App	equence 1, Appl	e 1,	equence 1,	equence 7,	(P)	equence 7,	equence 7,	e 7, Appl	e 894	equence 10	equence 41,	e 228	equence 41,	e 41, /	e 497, A	e 1, App	e 17607	equence 21	equence 66137,	equence 66	equence 66136,	equence 66135,	e 66138,	87, Ap

ALIGNMENTS

RESULT 1 US-09-949-016-1949

Sequence 1949, Appropriate Patent No. 681233

Application US/09949016

GENERAL INFORMATION: APPLICANT: VENTER, J.

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                              Alignment Scores:
Pred. No.:
                                                                             Score:
                                                                                                                                                         US-09-949-016-1949
                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-09-08
PRIOR FILLING DATE: 2000-09-08
                                                                                                                                                                                                                                    SOFTWARE: Fas
SEQ ID NO 1949
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATOR 1000-04-14
                                                                                                                                                                            LENGTH: 1260
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                       FastSEQ for Windows Version 4.0
1.99e-259
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100.0%
100.0%
90.6%
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Matches:
                  Mismatches:
Indels:
                                                          Conservative:
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Sequence 1, Application US/09127928
Patent NO. 6472172
Patent NO. 6472172
Patent NO. 6472172
Patent No. 6472172
PAPPLICANT: Deng, Gang
APPLICANT: Lin, Jiing-Huey
APPLICANT: Morser, Michael
TITLE OF INVENTION: DNA Encoding a No. 64721
TITLE OF INVENTION: Protein
FILE REFERENCE: DNA Encoding HIAP3
CURRENT APPLICATION NUMBER: US/09/127,928
CURRENT FILING DATE: 1998-07-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
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RESULT 3
US-09-949-016-13691
Sequence 13691, Application US/09949016
PARENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES AS:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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; LENGTH: 1337
; TYVER: DNA
; ORGANISM: Homo sap:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)...(:
US-09-127-928-1
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Best Local Similarity:
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RESULT 2 US-09-127-928-1

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APPLICANT: VULNTER, J. Craig et al.
APPLICANT: VULNTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 13691
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Best Local Similarity:
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US-09-949-016-13691
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                                                         SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 66130
LENGTH: 601
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TYPE: DNA
ORGANISM: Human
-09-949-016-66130
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Query Match:
                                                                                                                                                                         US-09-762-577B-12 (1-309) x US-09-949-016-66140 (1-601)
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US-09-949-016-66140
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66140, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 66140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS (
FILE REFERENCE: CLOOL307
CURRENT NEW TOTAL
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                                                                                                                   CCAGGAGCCAGGATGTGGAGGCGCAGCTGCGGCGGCTGCAGGAGGAGGACGTGCAAG
                                                                                                                                  ProGlyAlaArgAspValGluAlaGlnLeuArgArgLeuGlnGluGluArgThrCysLys
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Mismatches:
Indels:
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Matches:
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GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 66133, Application US/09949016
Patent NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN G.
TITLE OF INVENTION: WITH HUMAN DISEASE, MET
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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Best Local Similarity:
Query Match:
DB:
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US-09-949-016-66139
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Patent No. 6607879
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                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA
                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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Matches:
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Alignment Scores: Pred. No.:
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Best Local Similarity:
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Pred. No.:
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                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 66134
                                                                                                                              APPLICANTO NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 600-86
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                  Sequence 66134, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                      TYPE: DNA
ORGANISM: Human
                                                                                          LENGTH: 601
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
Query Match:
US-09-762-577B-12 (1-309) x US-09-016-434-216 (1-200)
                                                Query Match:
                                                                                                                                                           US-09-016-434-216
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                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-C
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 845-410
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                              LIBRARY: BLALLINE: 1520835
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CITY: PALO ALTO
                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALIFORNIA
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) 845-4166
- NO: 216:
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                                              Length:
Matches:
Conservative:
Mismatches:
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                                                                                              US-09-762-577B-12 (1-309) x US-09-023-655-387 (1-200)
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Best Local Similarity:
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                                                                                                                                              Query Match:
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US-09-023-655-387
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                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                              Alignment Scores:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 845-41 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERRNCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOO'D PEFFECT 6.1 for Windows/MS-DOS
CURRENT APPLICATION NUMBER: US/09/023,655
PILLING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
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APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                 No.:
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CITY: PALO ALTO
STATE: CALIFORNIA
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                                                    226 ArgArgLeuGlnGluGluArgThrCysLysValCysLeuAspArgAlaValSerIleVal
246 PheValProCysGlyHisLeuValCysAla 255
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                               40 CGGCGGCTGCAGGAGGAGGACGTGCAAGGTGTGCCTGGACCGCGCCGTGTCCATCGTC
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Sequence 66135, Application US/09949016

Retent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-09

PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-0-08

PRIOR FILING DATE: 2000-0-08

PRIOR FILING DATE: 2000-0-08
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PACENT NO. 6812339
PACENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER FILE REPERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                          Alignment Scores:
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; ORGANISM: Human
US-09-949-016-66135
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DB:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66135
LENGTH: 601
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Best Local Similarity:
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US-09-949-016-66138
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66138
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66136
Sequence 66331, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT ELLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
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US-09-949-016-66136
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Best Local Similarity:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001197

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 0000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-08

PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                    170 HisSerGlnLeuLeuGlySerTrp 177
                                                                                                                                                                                                                                                                                                                                                                            221 AGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGAGACTTTGTCCACAGTGTGCAGGAGACT
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Conservative:
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; ORGANISM: Human
US-09-949-016-66131
                                                                                                                US-09-762-577B-12 (1-309) x US-09-949-016-66137
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                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66137
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                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-010-03
PRIOR PRIOR DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66137
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
RUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66131
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 66137, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                        LENGTH:
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GCCCAGGAGCCAGGTGCA 426
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Mismatches:
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Gaps:
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Search completed: April 24, 2006, 10:02:44
Job time: 166 secs

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-Q=/abss/ABSSWEB_spool/US09762577/runat_24042006_105937_1201/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFWT=fastap_-SUFFIX=p2noli.rnpbm
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-VORDED-60 -VORDED-60 -VORDED-60 -VORDED-60 -FGAPOP=60 -FGAPOXT=7
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Maximum DB seq length: 200000000
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2: /cgm2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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10: /cgm2 6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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Ygapext 60.0
Fgapext 7.0
Delext 60.0
     US-10-244-586-2

US-10-108-646-4

US-10-807-897-28

US-10-244-586-1

US-10-108-646-12

US-10-807-897-26

US-10-235-026-1
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Sequence 2, Appli
Sequence 4, Appli
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ALIGNMENTS

RESULT 1 US-10-244-586-2

Sequence 2, Application US/10244586 Publication No. US20030087319A1

```
GENERAL INFORMATION:

APPLICANT: GOMES, BRUCE C.

APPLICANT: KASOF, GARRETT M.

APPLICANT: PROSSER, JUDITH C.

TITLE OF INVENTION: NOVEL PROTEIN

FILE REFERENCE: DJB/009901/0270799

CURRENT APPLICATION NUMBER: US/09/594,119

FRICR APPLICATION NUMBER: US/09/594,119

FRICR APPLICATION NUMBER: 60/139,291

PRIOR APPLICATION NUMBER: 60/139,291

PRIOR FILING DATE: 1999-06-15

NUMBER OF SEO ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 843

TYPE: DNA

ORGANISM: Homo sapiens

US-10-244-586-2

Alignment Scores: 2.67e-273

Pred. No.: 280.00

Percent Similarity: 100.0% Mismatches: 0

Percent Similarity: 100.0% Mismatches: 0

Dest Local Similarity: 100.0% Indels: 0

Query Match: 5

Gaps: 0
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RESULT 2
US-10-188-646-4
Sequence 4, Application US/10188646
Publication No. US20040005565A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0373
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-762-577B-12 (1-309)
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Publication No. US20040192631A1
GENERAL INFORMATION:
APPLICANT: Xiang, Rong
APPLICANT: Zhou, He
APPLICANT: Reisfeld, Ralph A.
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR
TITLE OF INVENTION: METHODS OF USE THEREOF
FILL REFERENCE: TSR1-874.1
CURRENT APPLICATION NUMBER: US/10/807,897
CURRENT APPLICATION NUMBER: 00/457,009
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 29
PRIOR FILING DATE: 203-03-24
NUMBER OF SEQ ID NOS: 29
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SEQ ID NO 28
LENGTH: 1268
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                                                                          TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
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Sequence 1, Application US/10244586
Publication No. US20030087319A1
GENERAL INFORMATION:
APPLICANT: GOMES, BRUCE C.
APPLICANT: KASOF, GARRETT M.
APPLICANT: PROSSER, JUDITH C.
APPLICANT: PROSSER, JUDITH C.
APPLICANT: PROSSER, JUDITH C.
CURRENT APPLICATION NUMBER: US/10/244,586
CURRENT FILING DATE: 2002-09-16
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US/09/594,119
RRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
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US-10-244-586-1
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TYPE: DNA
ORGANISM: Homo sapiens
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Alignment :
Pred. No.:
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
US-10-188-646-12
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Best Local Similarity:
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US-10-188-646-12
; Sequence 12, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
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APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
FILE REFERENCE: RTS-0373
CURRENT APPLICATION NUMBER: US/10/188,646
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 12
LENGTH: 1168
TYPE: DNA
ORGANISM: H. sapiens
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APPLICANT: Xiang, Rong
APPLICANT: Zhou, He
APPLICANT: Zhou, He
APPLICANT: Reisfeld, Ralph A.
TITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GROTITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TSRI-874.1
CURRENT APPLICATION NUMBER: US/10/807,897
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/457,009
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 1322
                                                                                                           ; LENGTH: 1322
; TYPE: DNA
; ORGANISM: homo sapi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...
                                         Alignment s
Pred. No.:
Score:
 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-10-807-897-26
; Sequence 26, Application US/10807897
; Publication No. US20040192631A1
; GENERAL INFORMATION:
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RESULT 7
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10235026 Publication No. US20030082725A1
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                               APPLICANT: Deng, Gang
APPLICANT: Lin, Jing-Huey
APPLICANT: Morser, Michael J
APPLICANT: Morser, Michael J
APPLICANT: Morser, Michael J
APPLICANT: MORSER, Michael J
TITLE OF INVENTION: DNA Encoding a No. US20030082725Alel Human Inhibitor-of-Apoptosis
FILE REFERENCE: 50972AUSD1
CURRENT FILING DATE: 2002-09-03
CURRENT APPLICATION NUMBER: US/10/235,026
CURRENT FILING DATE: 1998-07-31
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
                                                                        TYPE: DNA
ORGANISM: Homo
FEATURE:
         NAME/KEY: CDS
LOCATION: (170)..(1066)
OTHER INFORMATION:
                                                                                                                                         LENGTH: 1337
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US-10-839-882-37
; Sequence 37, Application US/10839882
; Publication No. US20040203106A1
; GENERAL INFORMATION:
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                                                               APPLICANT: INCYTE PHARMACEUTICALS, I.
APPLICANT: TANG, Y. TOM
APPLICANT: YUE, Henry
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: GUEGLER, Karl J.
APPLICANT: CORLEY, Wail C.
APPLICANT: LAL, Preeti
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
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      APPLICANT:
APPLICANT:
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No.:
ANT: TANG, Y. TOM
ANT: YUE, Henry
ANT: HILLMAN, Jennifer L.
ANT: GUEGLER, Karl J.
ANT: CORLEY, Neil C.
ANT: LAL, Preeti
ANT: LAL, Preeti
ANT: BAUGHN, Mariah R.
ANT: BAUGHN, Mariah R.
ANT: SHIH, Leo L.
DF INVENTION: PROLIFERATION AND PROLIFERATION PROLIFERATION AND PROLIFERATION PROLIFERATI
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SEQ ID NO 37
LENGTH: 1363
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SOFTWARE: PERL Program
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PRIOR FILING DATE: 1998-10-20; 1998-10-20; 1999-02-04; 1999-04-11; 1999-04-11; 1999-04-11;
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CURRENT APPLICATION NUMBER: US/10/839,882
CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: US/09/807,452
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/175,737; unassigned; 60/118,559; 09/249,740; unassigned;
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID
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ORGANISM: Homo
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                       LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGly 217
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                                                                                                                       AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp
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SEQ ID NO 21
TRNGTH: 1068
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US-10-203-708-21
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER: OF SEQ ID NOS: 46
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Publication No. US20030149238A1
GRMERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.1.C.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
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GACTTTGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCCTGG
                                 AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrp
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                                                                                               TGGACGGAGCATGCCAAGTGGTTCCCCCAGCTGTCAGTTCCTGCTCCGGTCAAAAGGAAGA
                                                                                                                              TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
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Query Match:
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; ORGANISM: Homo
US-10-723-860-4697
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US-10-203-708-22
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                           Sequence 22, Application US/10203708
Publication No. US20030149238A1
GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.l.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
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APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
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Sequence 8265, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginchik, Albert
TITLE OF INVENTION: Methods of Diagnosis of S.
TITLE OF INVENTION: Methods For Screening fo
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR FILING DATE: 2002-11-26
PRIOR FILING DATE: 2002-11-26
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US-10-723-860-8265
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; ORGANISM: Homo
US-10-203-708-22
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 769
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                                                                   TrpThrGluHisAlaLysTrpPhePro 149
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f Soft Tissue Sarcoma, Compositions for Soft Tissue Sarcoma Modulators

NUMBER OF SEQ ID NOS: 8393

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CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT PILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSECUM
SOFTWARE: CUSECUM
CORGANISM: Homo Sapiens
PEATURE: DNA
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSECUM
CORGANISM: Homo Sapiens
PEATURE: DNA
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; ORGANISM: Homo
US-10-723-860-8265
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Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
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SEQ ID NO 8265
LENGTH: 858
NAME/KEY: SIMILAR
LOCATION: (309)..(614)
COTHER INFORMATION: 35% homologous to Homo sapiens inhibitor of apoptosis protein
OTHER INFORMATION: KIAP, accession number AF301009, Smith-Waterman Score=86.
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Best Local Similarity:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-63
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TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 764PCT
CURRENT APPLICATION NUMBER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 63
TENCRU. 616
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Publication No. US20040053248A1
GENERAL INFORMATION:
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RESULT 15
US-10-188-646-11
US-10-188-646-11
Sequence 11, Application US/10188646
Publication No. US20040005565A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Doble
TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
FILE REFERENCE: RTS-0373
CURRENT APPLICATION NUMBER: US/10/188,646
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4810
TYPE: DNA
ORGANISM: H. sapiens
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                                                                                                                                         43
                                                                                                                                                                                    41 GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
                                                                                                                                                                                                                                         21 AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
                                                                                                                              ProLeuThrGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
                                                                                                                                                                                                                          GCCGGTGATGGTCCCACGCAGGAGCGCTGTGGACCCCGCTCTCTGGGCAGCCCTGTCCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCAGGACAAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrProGluLeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGly 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspProTrpGluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGly 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGACCCCTGGACGGAGCATGCCAAGTGGTTCCCCAGCTGTCAGTTCCTGCTCCGGTCA
                                                                                                             CCCCTGACAGAGGAGGAAGGAGGAGGGCGCCGGGGCCACCTTGTCCAGGGGGCCTGCC 549
                                                                                                                                                                    GGCCTGGACACCTGCAGAGCCTGGGACCACGTGGATGGGCAGATCCTGGGCCAGCTGCGG
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117.00
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100.0%
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Search completed: April 24, 2006, 10:13:42

Job time : 631 secs

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Result
No.
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-MODEL-frame-p2n.model -DEV=xlh
-Q-/abss/ABSSWEB spool/US09762577/runat 24042006 105939 1250/app_query.fasta_1
-Q-/abss/ABSSWEB spool/US09762577/runat 24042006 105939 1250/app_query.fasta_1
-DB=Published Applications_NA_New -QFMT=fastap -SUFFIX=p2noli.rnpbn
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -THR MIN=1
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -QUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss056
-MAXLEN=2000000000 -HOST=abss056
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -USER=US09762577 @CGN 1_1_545_@runat_24042006_105939_1250 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WAEN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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     NH
                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                          Score
     177
149
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                                                     Query
Match Length DB ID
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Ygapop 60.0
Fgapop 60.0
Delop 60.0
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1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*

2: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*

3: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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  57.3
48.2
                                                                                                                                                                                                                                                                                       /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
/SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
/SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
/SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
/SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
1: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
2: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
3: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
4: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
4: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
5: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
  1068
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US-11-135-855-21
US-11-135-855-22
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                                                                     Description
Sequence 21,
Sequence 22,
App1
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ALIGNMENTS

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RESULT 1
US-11-135-855-21
US-11-135-855-21
Sequence 21, Application US/11135855
Publication No. US2005025557A1
GENERAL IMPORWATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM P.L.C.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
CURRENT APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2002-08-13
PRIOR FILING DATE: 2001-02-14
PRIOR PILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
SOFTWARE: FRANCE: GRANGE VERSION 3.0
SEQ ID NO 21
LENGTH: 1068
TYPE: DNA
ORGANIZM: Homo sapiens
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APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM p.1.c.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50013
CURRENT FILING DATE: 2005-05-24
PRIOR APPLICATION NUMBER: US/11/135,855
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/10/203,708
PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/US01/04703
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,172
PRIOR PILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/186,084
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FRASESEQ for Windows Version 3.0
SEQ ID NO 22
TYPE: DATE: 769
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US-11-135-855-22
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/11135855 Publication No. US20050255557A1 GENERAL INFORMATION:
         LENGTH: 769
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
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                                                                                                                                                                                                                                                                                                                                                                                                                GACTTTGTCCACAGTGTGCAGGAGACTCACTCCCAGCTGCTGGGCTCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro
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APPLICANT: MILLER, LANCE D.
APPLICANT: MILLER, LANCE D.
APPLICANT: VEGA, VINSENSIUS B.
TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
TITLE OF INVENTION: PROGNOSIS, AND DIAGNOSIS OF CANCERS
FILE REFERENCE: 38271-76067
CURRENT APPLICATION NUMBER: US/10/960,414
CURRENT APPLICATION NUMBER: US/10/960,414
CURRENT FILING DATE: 2004-10-06
NUMBER OF SEQ ID NOS: 500
SOFTWARE: Patentin version 3.3
SEQ ID NO 432
LENGTH: 3076
TYPE: DNA
CRGANISM: Homo sapiens
US-10-960-414-432
                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                            RESULT 3
US-10-960-414-432
US-10-960-414-432
; Sequence 432, Application US/10960414
; Publication No. US20060074565A1
; GENERAL INFORMATION:
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US-09-762-577B-12 (1-309)

x US-10-960-414-432 (1-3076)

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Best Local Similarity:
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                                                          Percent Similarity:
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APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT EILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 2596
LENGTH: 3837
                                                                                                                                                                                                              APPLICANT: Wyeth
APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6853
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6853, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
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                                                                                                                                                                    TYPE: DNA ORGANISM: Rattus norvegicus
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                            LENGTH: 600
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Query Match:
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Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILLE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILLING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION DATE: 2002-08-09
PRIOR APPLICATION DATE: 2002-08-09
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PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39825
LENGTH: 1257
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 653234, Application US/10301480 Publication No. US20060057564A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                           SEQ ID NO 653234
                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR PILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                              ORGANISM: Homo sapien
                                                                                                                                                                                                   LENGTH: 1257
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 LeuGlnGluGluArgThrCysLysValCys 237
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Matches:
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Matches:
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APPLICANT: Wyeth

APPLICANT: Mounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR FILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

SEQ ID NO 303

LENGTH: 2468

TYPE: DNA

COMMANDER PATENTS Norvegicus
US-09-762-577B-12 (1-309) x US-11-136-527-303 (1-2468)
                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                       Pred. No.:
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// ORGANISM: Rattus norvegicus
US-11-136-527-303
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Best Local Similarity:
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; ORGANISM: Rattus norvegicus
US-11-136-527-2757
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US-11-136-527-2757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 303, Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIN version 3.2
SEQ ID NO 2757
LENGTH: 2106
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Publication No. US20050287570A1
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APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
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Indels:
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Matches:
Conservative:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS AS TITLE OF INVENTION: CARDIOVASCULAR DISORDER TITLE OF INVENTION: DETECTION AND USES THEF FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63908
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                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
 RESULT
                                                                                           US-09-762-577B-12 (1-309)
                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-10-995-561-64173
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US-10-995-561-63908/c
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 65702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 64173
LENGTH: 201
TYPE: DNA
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Publication No. US20050272054A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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12
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                                                     37 SerProValLeuGlyLeuAspThrCys 45
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GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
DETECTION AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 5527
LENGTH: 599
TYPE: DNA
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CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1885
LENGTH: 599
TYPE: DNA
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US-11-128-061-5527
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Best Local Similarity:
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APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES RELATED TO OLIGONUCLECTIDE ARRAYS
FILE REFERENCE: 0.1997.027701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sinacore, Martin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
FILE REFERENCE: 01997.027701
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APPLICANT: Charlebois, Timo
APPLICANT: Mounts, William |
APPLICANT: Hann, Louane E.
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NAME/KEY: misc feature
LOCATION: (26)..(71)
                                                                             ORGANISM: Cricetulus griseus
NAME/KEY: misc_feature
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US-11-128-049-5527
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Best Local Similarity:
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Best Local Similarity:
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APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO
TITLE OF INVENTION: MAKING AND USING SAME
FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
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Sequence 5527, Application US/11128049 Publication No. US20060010513A1
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Publication No. US20060010513A1
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APPLICANT:
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APPLICANT: Charlebois, Timothy
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane E.
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OTHER INFORMATION: n is a,
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LOCATION: (26)..(71)
OTHER INFORMATION: n is a,
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TYPE: DNA
ORGANISM: Cricetulus griseus
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                                                                                        163
                                                                                                           245 ValPheValProCysGlyHisLeuVal 253
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Leonard, Mark W.
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GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timot
APPLICANT: Mounts, William N
APPLICANT: Hann, Louane E.

Charlebois, Timocus Mounts, William M.

Timothy S

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APPLICANT: Sinacore, Markin S.
APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLECTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR TITLE OF INVENTION: MAKING AND USING SAME
FILE REPERENCE: 0.1997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT APPLICATION NUMBER: US/570,425
PRIOR FILING DATE: 2004-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
INUMBER OF SEQ ID NOS: 7285
SOFTWARE: Patentin version 3.3
SEQ ID NO 5527
LENGTH: 599
TYPE: DNA
ORGANISM: Cricetulus griseus
FEATURE:
NAME/KEY: misc_feature
LCCATION: (26)...(71)
OTHER INFORMATION: n is a, c, g, or t
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Best Local Similarity:
Query Match:
DB:
Search completed: April 24, 2006, 10:45:06 Job time : 1858 secs
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                                                                                       245 ValPheValProCysGlyHisLeuVal 253
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Matches:
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Mismatches:
Indels:
Gaps:
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-10-553-355-11	US-10-188-646-4	US-10-170-235-27143	PCT-US03-20821-4	PCT-US99-17738-11	US-10-244-586-2	US-09-594-119-2	ID
Sequence 11, Appl	Sequence 4, Appli	Sequence 27143, A	Sequence 4, Appli	Sequence 11, Appl	Sequence 2, Appli	Sequence 2, Appli	Description

240 80

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Sequence 2, Application US/09594119
GENERAL INFORMATION:
APPLICANT: GOMES, BRUCE C.
APPLICANT: KASOF, GARRETT M.
APPLICANT: KASOF, GARRETT M.
APPLICANT: PROSSER, JUDITH C.
TITLE OF INVENTION: NOVEL PROTEIN
FILE REFERENCE: DIB/009901/0270799
CURRENT APPLICATION NUMBER: US/09/594,119
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 60/139,291
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 843
TYPE: DNA
ORGANISM: Homo sapiens
US-09-594-119-2
                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                           Alignment & Pred. No.:
                                          US-09-762-577B-12 (1-309) x US-09-594-119-2 (1-843)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-09-594-119-2
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16 US-10-940-774A-1949
17 US-10-940-774A-1949
18 PCT-US02-29560A-182
18 PCT-US02-29560A-182
19 PCT-US02-29560A-182
29 PCT-US02-29560A-182
20 US-10-867-897-28
20 US-0-685-372-1130
20 US-60-680-544-45583
20 US-60-680-544-45583
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Sequence 1949, Ap
Sequence 182, App
RESULT 2
US-10-244-586-2
US-10-244-586-2
; Sequence 2, Application US/10244586
; GENERAL INFORMATION:
; APPLICANT: COMES, BRUCE C.
; APPLICANT: HASOF, GARRETT M.
APPLICANT: PROSSER, JUDITH C.
; APPLICANT: PROSSER, JUDITH C.
; TITLE OF INVENTION: NOVEL PROTEIN
FILE REFERENCE: DJB/009901/0270799
; CURRENT APPLICATION NUMBER: US/10/244,586
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/9/594,119
; PRIOR APPLICATION NUMBER: US/9/594,119
; PRIOR APPLICATION NUMBER: 05/9/594,119
; PRIOR APPLICATION NUMBER: 05/9/594,119
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver: 2.1
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; SEQ ID NO 2
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Sequence 11, Application PC/TUS9917738

Sequence 11, Application PC/TUS9917738

GENERAL INFORMATION:

APPLICANT: Dranoff, Glenn

APPLICANT: Schmollinger, Jan

APPLICANT: Hodi, F. Stephen

APPLICANT: Mollick, Joseph

TITLE OF INVENTION: TUMOR ANTIGENS AND USES THE

FILE REFERENCE: 50059/005W02

CURRENT APPLICATION NUMBER: PCT/US99/17738

CURRENT APPLICATION NUMBER: 60/095,766

EARLIER APPLICATION NUMBER: 60/095,766

EARLIER FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 11

LENGTH: 1246

TYPE: DNA

ORGANISM: Homo sapiens
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Query Match:
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LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGlyAlaArgAsp
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                                                                 LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro
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Gaps:
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Sequence 4, Application PC/TUS0320821
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
ITILE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXI
FILE REFERENCE: ISISO37-500
CURRENT APPLICATION NUMBER: PCT/US03/20821
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION UNMBER: US 10/188,646
PRIOR APPLICATION UNMBER: US 10/188,646
NUMBER OF SEQ ID NOS: 153
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Pred. No.:
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PCT-US03-20821-4
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NAME/KEY: CDS
LOCATION: (174
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ORGANISM: H. sapiens
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Sequence 27143, Application:

APPLICANT: VENTER, J. Craig

APPLICANT: VENTER, J. Craig

TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF

FILE REFERENCE: CL001380

CURRENT APPLICATION NUMBER: US/10/170,235

CURRENT FILING DATE: 2003-03-17

NUMBER OF SEQ ID NOS: 42514

SEQ ID NO 27143

LENGTH: 1260

TYPE: DNA

ORGANISM: HUMAN

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            CCCCTGACAGAGGAGGAGGAGGAGGAGGGCGCCGGGGCCACCTTGTCCAGGGGGCCTGCC
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Sequence 4, Application US/10188646
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: K. Genneth W. Dobie
TITLE OF INVENTION: ANTISHNSE MODULATION OF
FILE REFERENCE: RTS-0373
CURRENT FPLICATION NUMBER: US/10/188,646
CURRENT FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 4
                                              Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-188-646-4
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                                                                                                                                                        TYPE: DNA ORGANISM: H. FEATURE:
                                                                                                                            NAME/KEY: CDS
LOCATION: (174)...
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Kenneth W. Dobie
ENTION: ANTISENSE MODULATION OF LIVIN
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Matches:
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RESULT 7

US-10-553-355-11

US-10-553-355-11

Sequence 11, Application US/10553355

GENERAL INFORMATION:

APPLICANT: Deutsches Krebsforschungszentrum

ITITLE OF INVENTION: Livin-specific sirnas for the

FILE REFERENCE: DK62169PC

CURRENT APPLICATION NUMBER: US/10/553,355

CURRENT FILING DATE: 2005-10-14

PRIOR APPLICATION NUMBER: EP 0300 8081.6

PRIOR FILING DATE: 2003-04-15

NUMBER OF SEQ ID NOS: 11
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo :
US-10-553-355-11
                                                                    SEQ ID NO 11
                                                                                       SOFTWARE: Patentin
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RESULT 8
US-10-940-774-1949
; Sequence 1949, Application US/10940774
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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CURRENT APPLICATION NUMBER: US/10/940,777;
CURRENT FILING DATE: 2004-09-15

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

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Sequence 1949, Application US/10940774A

Sequence 1949, Application US/10940774A

GENERAL INFORMATION: FOLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/10/940,774A

CURRENT FILING DATE: 2004-09-15

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING 
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; ORGANISM: Human
US-10-940-774A-1949
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US-10-940-774A-1949
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                                                                                     Ly8ValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
                                                                                                                                                               GCTGAGGTGCCACCCGAGCTGCTGGCTGCCGGCTTCTTCCACACAGGCCATCAGGAC 533
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                                                         AAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCC 593
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APPLICANT: Mack, David H.
APPLICANT: Wilson, Keith E.
APPLICANT: Zlotnik, Albert
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710PC
CURRENT APPLICATION NUMBER: PCT/JS02/29560
CURRENT FILING DATE: 2025-11-01
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 412
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 182
LENGTH: 1268
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-29560-182
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PCT-US02-29560-182
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APPLICANT: Aziz, Natash,
APPLICANT: Gish, Kurt C
APPLICANT: Hevezi, Pete;
APPLICANT: Mack, David I
APPLICANT: Wilson, Keitl
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GlyLeuAspThrCysArgAlaTrpAspHisValAspGlyGlnIleLeuGlyGlnLeuArg
                                                                                        AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu
                                                                                                                                                             ATGGGACCTAAAGACAGTGCCAAGTGCCTGCACCGTGGACCACAGCCGAGCCACTGGGCA
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Gish, Kurt C.
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SEQUENCE 182, Application PC/TUS0229560A

SEQUENCE 182, Application PC/TUS0229560A

GENERAL INFORMATION:

APPLICANT: Afar, Daniel

APPLICANT: Afar, Daniel

APPLICANT: Hevezi, Peter A.

APPLICANT: Hevezi, Peter A.

APPLICANT: Walson, Keith E.

APPLICANT: Zlotnik, Albert

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of CINERENT EFERENCE: 018501-002710PC

CURRENT APPLICATION NUMBER: PCT/US02/29560A

CURRENT FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: US 60/323,469

PRIOR FILING DATE: 2001-09-17

PRIOR FILING DATE: 2001-09-17

SOFTWARE: FRatSEQ for Windows Version 3.0

CURGITH: 1268

TYPE: DNA

CORGANISM: Homo sapiens

PCT-US02-29560A-182
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PCT-US02-29560A-182
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RESULT 12

PCT-US04-08932-28

; Sequence 28, Application F
; GENERAL INFORMATION:
; APPLICANT: Xiang, Rong
; APPLICANT: Zhou, He
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APPLICANT: Reisfeld, Ralph A.
APPLICANT: The Scripps Research Institute
ITITLE OF INVENTION: DNA VACCINES AGAINST TUMOR GRC
ITITLE OF INVENTION: METHODS OF USE THEREOF
ITILE REFERENCE: TSRI-874.1PC
CURRENT APPLICATION NUMBER: PCT/US04/08932
CURRENT FILING DATE: 2004-03-29
PRIOR APPLICATION NUMBER: 60/457,009
PRIOR APPLICATION NUMBER: 60/457,009
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 1268
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ORGANISM: homo
GluGluProGluAspAlaAlaProValAlaProSerValProAlaSerGlyTyrProGlu
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APPLICANT: Mack, David H.

APPLICANT: Wilson, Kelth E.

APPLICANT: Wilson, Kelth E.

APPLICANT: Zotnik, Albert

ITILE OF INVENTION: Methods of Streening for Modulators of Cancer

ITILE OF INVENTION: Methods of Streening for Modulators of Cancer

FILE REFERENCE: 018501-002710US

CURRENT APPLICATION NUMBER: US/10/245,882

CURRENT FILING DATE: 2002-12-13

PRIOR APPLICATION NUMBER: US 60/323,469

PRIOR APPLICATION NUMBER: US 60/323,469

PRIOR APPLICATION NUMBER: US 60/323,887

PRIOR APPLICATION NUMBER: US 60/323,887

PRIOR APPLICATION NUMBER: US 60/325,114

PRIOR APPLICATION NUMBER: US 60/325,114

PRIOR APPLICATION NUMBER: US 60/325,114

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR APPLICATION NUMBER: US 60/355,145

PRIOR APPLICATION NUMBER: US 60/355,145

PRIOR APPLICATION NUMBER: US 60/355,257

PRIOR APPLICATION NUMBER: US 60/352,246

PRIOR APPLICATION NUMBER: US 60/355,257
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; TYPE: DNA
; ORGANISM: Homo s
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US-10-245-882-182
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SOFTWARE: FASTSEQ for Windows
SEQ ID NO 182
LENGTH: 1268
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                        AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu
                                                                                                                  MetGlyProLysAspSerAlaLysCysLeuHisArgGlyProGlnProSerHisTrpAla
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Gish, Kurt C.
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Alignment Scores: Pred. No.: PCT-US04-08932-28

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RESULT 14
US-10-807-897-28
(Sequence 28, Application US/10807897
(GENERAL INFORMATION:
APPLICANT: Xiang, Rong
APPLICANT: Xiang, Rong
APPLICANT: Reisfeld, Ralph A.
APPLICANT: Reisfeld, Ralph A.
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TSR1-874.1
CURRENT APPLICATION NUMBER: US/10/807,897
CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/457,009
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 1268
TYPE: DNA
ORGANISM: homo sapiens
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NAME/KEY:
LOCATION:
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RESULT 15
US-60-655-372-1181
; Sequence 1181, Application
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; APPLICANT: Belouchi, Abdel
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; ORGANISM: Homo sapiens
US-60-685-372-1181
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APPLICANT: Cousineau, Johanne
APPLICANT: Berdewegh, Paul V
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: Genemap of the Human Genes Associated with Psoriasis
FILE REFERENCE: 059908-5005-PR
CURRENT APPLICATION NUMBER: US/60/685,372
CURRENT FILING DATE: 2005-05-31
NUMBER OF SEQ ID NOS: 2738
SOFTWARE: Patentin version 3.3
SEQ ID NO 1181
LENGTH: 1268
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Nguyen-Huu, Quynh
Croteau, Pascal
Allard, Rene
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                                                                             AspPheValHisSerValGlnGluThrHisSerGlnLeuLeuGlySerTrpAspProTrp 180
                                                                                                                                 TrpThrGluHisAlaLysTrpPheProSerCysGlnPheLeuLeuArgSerLysGlyArg 160
                                                                                                                                                                                                                                                           AlaGluValProProGluLeuLeuAlaAlaAlaGlyPhePheHisThrGlyHisGlnAsp 120
                                                                                                                                                                                                                                                                                                               PheProGlyMetGlySerGluGluLeuArgLeuAlaSerPheTyrAspTrpProLeuThr 100
                                                                                                                                                                                                                                                                                                                                                                   ProLeuThrGluGluGluGluGluGluGlyAlaGlyAlaThrLeuSerArgGlyProAla 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaGlyAspGlyProThrGlnGluArgCysGlyProArgSerLeuGlySerProValLeu
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\texttt{LeuProThrProArgArgGluValGlnSerGluSerAlaGlnGluProGlyAlaArgAsp}
                                                                                                                                                                                      AAGGTGAGGTGCTTCTTCTGCTATGGGGGCCTGCAGAGCTGGAAGCGCGGGGACGACCCC
                                                                                                                                                                                                           LysValArgCysPhePheCysTyrGlyGlyLeuGlnSerTrpLysArgGlyAspAspPro 140
                                                                                                                                                                                                                                                                                                                                                    CCCCTGACAGAGGAGGAGGAGGAGGCCCCCGGGGCCACCTTGTCCAGGGGGCCTGCC 413
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Bradley, Walter E
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Matches:
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Search completed: April 24, 2006, 11:51:02 Job time: 6656 secs THIS PAGE BLANK (USPTO)

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Result
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-MODEL=frame+ p2n.model -DEV=xlp
-O=labss/BASSWEB spool/US09762577/runat 24042006 105934 1148/app query.fasta_1
-O=labss/BASSWEB spool/US09762577/runat 24042006 105934 1148/app query.fasta_1
-DB=Pending_Patents_NA_New -OFMT=fastap_-SUFFIX=p2no11.rnpn -MINNATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -LEND=-1 -MATRIX=001igo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abss03p
-USER=US09762577 @CGN 1 1 803 @runat 24042006 105934 1148 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                                                                            Score
         280
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1: /SIDS5/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /SIDS5/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /SIDS5/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /SIDS5/ptodata/2/pna/US08_NEW_COMB.seq:*

4: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq:*

5: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq:*

6: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq:*

7: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq:*

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12: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq2:*

13: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq3:*

13: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq3:*

14: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq3:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Sequence 11, Appl
Sequence 23550, A
Sequence 290500,
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212950, 26831, 1159, Ap 3, Appli	726, 726, 726 8053 726 8053 73133 743184	Sequence 1867; equence 41, A; Sequence 41, A; Sequence 7, Ap; sequence 7, A; Sequence 5904; Sequence 1981	equence 4 equence 2 equence 2 equence 3 equence 3 equence 6	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	equence 34192 equence 23135 equence 49, Ap equence 41998 equence 11520 equence 27179 equence 13179 equence 11533 equence 115770

ALIGNMENTS

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US-09-762-577B-11

Sequence 11, Application US/09762577B

Sequence 11, Application US/09762577B

SEQUENCAL INFORMATION:

APPLICANT: Dranoff, Glenn
APPLICANT: Schmollinger, Jan
APPLICANT: Modi, F. Stephen
APPLICANT: Mollick, Joseph
TITLE OF INVENTION: TUMOR ANTIGENS AND USES THEREOF
FILE REFERENCE: 2486/109
CURRENT APPLICATION NUMBER: US/09/762,577B
CURRENT FILING DATE: 2002-08-29
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 68
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1246
TYPE: DNA
CORGANISM: homo sapiens
US-09-762-577B-11
Alignment Scores:
Pred. No.:
CORGANISM: Applicative: 5.35e-267
Percent Similarity: 100.0%
Mismatches: 0
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RESULT 2
US-11-266-748A-23550
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Sequence 2350, Application US/11266748A
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR PPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PRIOR PRIOR PRIOR 11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PRIOR DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER: OF CEO. TO NOO.
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SEQ ID NO 23550
LENGTH: 1260
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ORGANISM: Homo
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GAAGAACCGGAAGACGCAGCCCCTGTGGCCCCCTCCGTCCCTGCCTCTGGGTACCCTGAG
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105484.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
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US-11-266-748A-290500
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US-11-266-748A-290500
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SEQ ID NO 290500
LENGTH: 1000
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GENERAL INFORMATION:
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PRIOR FILING DATE: 2005-07-18
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                                            GGGCAGATCCTGGGCCCAGCTGCGGCCCCTGACAGAGGAGGAAGAAGAGGAGGAGGACGCCCGGG
                                                                                                      CGCTCTCTGGGCAGCCCTGTCCTAGGCCTGGACACCTGCAGAGCCTGGGACCACGTGGAT
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APPLICANT: Johnsto
APPLICANT: Mulliga
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2005-03-14

PRIOR FILING DATE: 2005-03-14
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3
SEQ ID NO 341929
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Mulligan, Karl
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RESULT 5
US-11-266-748A-211754/c
; Sequence 211754, Application U
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
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RESULT 6
US-11-266-748A-235360
Sequence 235360, Application US/11266748A
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray
TITLE OF INVENTION: Methods of Using the Sar
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ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 489996
SOFTWARE: Patentin version 3.3
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Microarray Technology

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Percent Similarity:
Best Local Similarity:
Query Match:
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TYPE: DNA;
ORGANISM: Homo Sapiens
US-11-266-748A-235360
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CCURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
NUMBER: DATE: 1005-07-18
NUMBER: DATE: 1005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-762-577B-12 (1-309) x US-11-266-748A-235360 (1-633)
Sequence 49, Application US/09762577B
GENERAL INFORMATION:
APPLICANT: Dranoff, Glenn
APPLICANT: Schmollinger, Jan
APPLICANT: Hodi, F. Stephen
APPLICANT: Mollick, Joseph
TITLE OF INVENTION: TUMOR ANTIGENS AND USES THEREOF
FILE REFERENCE: 2486/109
CURRENT APPLICATION NUMBER: US/09/762,577B
CURRENT FILING DATE: 2002-08-29
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Undinston, Patrick
APPLICANT: Willigan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-07-18
                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                  ; ORGANISM: Homo Sapiens
US-11-266-748A-41998
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US-11-266-748A-41998
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NAME/KEY: misc feature
LOCATION: 163, 168
OTHER INFORMATION: n =
US-09-762-577B-49
  US-09-762-577B-12 (1-309) x US-11-266-748A-41998 (1-634)
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LENGTH: 634
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PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 49
                                                                                                                                                                                                                                                                                    LENGTH: 63
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TYPE: DNA
ORGANISM: homo sapiens
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Alignment Scores:

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RESULT 7 US-09-762-577B-49

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Percent Similarity:
Best Local Similarity:
Query Match:
                                               US-09-762-577B-12 (1-309) x US-11-266-748A-15520 (1-927)
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US-11-266-748A-15520
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PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR HILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR PELICATION NUMBER: EP 04105485.9
PRIOR PELICATION NUMBER: EP 04105485.9
PRIOR PELICATION NUMBER: EP 04105485.9
PRIOR PELICATION NUMBER: EP 04105484.2
PRIOR PELICATION NUMBER: BP 04105484.2
PRIOR APPLICATION NUMBER: US 06/662,276
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 06/662,276
PRIOR FILING DATE: 2005-03-14
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 15520
LENGTH: 927
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NAME/KEY: misc feature
LOCATION: (641)..(696)
OTHER INFORMATION: n is a
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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224 GlnLeuArgArgLeuGlnGluGluArgThrCysLysValCys
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Mulligan, Karl
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; FRATURE:
; NAMB/KEY: misc feature
; LOCATION: (887)...(887)
; OTHER INFORMATION: n is
US-11-266-748A-21170
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PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-18
PRIOR PILING DATE: 2005-03-19
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2004-11-03
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RESULT 11
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Best Local Similarity:
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APPLICANT: Harkin, Paul APPLICANT: Johnston, PAPPLICANT: Johnsto
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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NAME/KEY: misc feature
LOCATION: (641)...(696)
OTHER INFORMATION: n is
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ORGANISM: Homo Sapiens
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LOCATION: (800)..(800)
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LOCATION: (712)...(712)
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
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US-11-266-748A-115538
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Best Local Similarity:
Query Match:
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US-11-266-748A-13769
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PRIOR FILING DATE: 2004-11-03
PRIOR PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology in ITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT PILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105479.2
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PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
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US-09-762-577B-12 (1-309) x US-11-266-748A-157702 (1-1000)
                                                                                Percent Similarity:
Best Local Similarity:
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SEQ ID NO 157702
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 115538
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
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APPLICANT: Johnston, P
APPLICANT: Mulligan, K
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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TYPE: DNA
ORGANISM: Homo Sapiens
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FILING DATE: 2004-11-03
APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
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Mulligan, Karl
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224 GlnLeuArgArgLeuGlnGluGluArgThrCysLysValCys 237

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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: $5815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PRILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105403.4
PRIOR APPLICATION NUMBER: EP 04105507.0
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
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DB:
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; ORGANISM: Homo Sapiens
US-11-266-748A-220957
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Sequence 220957, Ap
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APPLICANT: Harkin, Paul
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Query Match:
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US-11-266-748A-224572
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PRIOR FILLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILLING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILLING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 224572
LENGTH: 1000
TYPE: DNA
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                                                                                               224 GlnLeuArgArgLeuGlnGluGluArgThrCysLysValCys 237
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